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Nagase, T., Ishikawa, K., Nakajima, D., Ohira, M., Seki, N., Miyajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O. Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro
DNA Res. 4 (2), 141-150 (1997)
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Chara,O., Nagase,T., Kikuno,R. and Nomura,N.
Direct Submission
Submitted (28-MAR-1997) Osamu Ohara, Kazusa DNA Research Institute;
1532-3; Yana, Kisarazu, Chiba 292-0812, Japan
(R-mail:cdnainf@kazusa.or.jp, Tel:+81-438-52-3913)
Location/Qualifiers
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C0889125 Sequence
BD157975 Primer fo
AX879698 Sequence
AX022734 Homo sapi
BT010098 Drosophil
AX090879 Homo sapi
AL512385 Human DNA
C0289124 Sequence
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AC01037 Drosophil
AC10037 Drosophil
AX113004 Ciona int
AX113004 Ciona int
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AX13004 Ciona int
AX13006 Seallus ga
BC007645 Homo sapi
AX1259699 Mouse DNA
AX125756 Rattus no
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/CgnZ 1/USFO spool p/USIOT64390/runat 12102005 110203 22329/app query.fasta_1.1223
-Q=/CgnZ 1/USFO spool p/USIOT64390/runat 12102005 110203 22329/app query.fasta_1.1223
-DB=GenEmbl -QFWT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LGOPCL=0 -LGOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-PEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd.
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GSPEGIWGDSPEDIRKDLFFGKDWGLERMSEYADDYRELEKDLLQPSGKQDERGSAB
YTDWGLLPGSEGAFNSSVGDSPAVPAETQOPPELHYLNESASTPAPKLPERSVLLPLP
TYPSSGEVLEKERASQUGGGSSNSSGREVLMPSHSLPPASLELSSYTVRKSPYLTVTP
TYPSSGEVLEKERASQUGGGSSNSSGREVLMPSHSLPTSALITSPUSYTVTSSEN
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AFVARAPPVETTYNYREWIL: SPHTDYGGEIRIGHTGAPKGTINLSQLSVGTVYFWSEN
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VAANGPHTITLOGNSITLAKSNLDPGNSFRLLYTDSDGATNSTTAALIVNNAUDYPP
VAANGPHTITLOGNSITLAKSROSSDHQIVLYVIVQPENNRPPVAVGFDKELIFPVRGGSSSSBDHGIYFYLHG
SANGGEDTTFOLKYTDSSRQCSTAVTVIVQDENNRPPVAVGFDKELIFPVRGGSSS
TSTLLYVAVKKENNSPPRARAGGRRHULVLPNNSSTLLDGSRSTDDQRIVSYTHTRDGGSP
                                                                                                                                                                                                                                                                                                                                                                               AAGDVI DGSDHSVALQLTNILVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVE
LTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKI RAHSDLSTV VFYVQSRPPR
KVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLFKRCTCSHL
KWTSTALDNT I WDGESNCEMSI FYVTVLAFTLI VLTGGFTWLCI CCCKRQKRTKIRKKT
KWTI LDNMDEQERMBLARKYGIKHRSTEHNSSLMVSESEFDSDQDTIFSREKMERGNP
KVSMNGSI RNGASFSYCSKDR"
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                                                                                                                                             not identified
                                                                              plus"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                              SK
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/organism="Homo sapiens"
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5574.00
99.72%
99.72%
                                                    /sex="male"
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Best Local Similarity
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1035 GAAGAGACTTTACAGCTCCAAGAACAACCGAGGAATAGCTCTGGAAAAGAGGTTCCAATG 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 AlaAlaProSerGluSerThrProSerGluLeuProIleSerProThrThrAlaProArg 330
                                                                                                                                     Leu***PheLeuGlyLysAspTrpGlyLeuGluGluMetSerGluTyr***AspAspTyr 160
                                                                                                                                                                                                                    ArgGluLeuGluLysAspLeuLeuGlnProSerGlyLysGlnGluProArgGlySerAla 180
                                                                                                                                                                                                                                                                                                   GluTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsn---SerSerVal 199
                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGACAACTCAGCTGCATGGAGAAGCTGCAGGATCCCACGCCCCACCACTGGAC 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1095 CCTTCCCATAATCCTTCCCCTGCCAGCCTGGAGTCTAGCCCAGCCACGAAAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1452 CCGACTCTTCACCTCTCAATTATCTGTGGGACTCTATGCCTTCAGAGTGGCTGTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluTrpAsnLeulleSerHisProThrAspTyrGlnGlyGluIleLysGlnGlyHisLys
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LeudendrygGlySerProSerGlyIleTrpGlydspSerProGludspIledrygLysAsp
                                                                                 -----GluLeuHisTyrLeuAsnGluSerAlaSerThrProAlaProLysLeuProGlu
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KVLKVDTAGGLLKCSGHGHCDP I TKRCI CSQLWHENL I QRYWNDGESNUEWSVFYVAA
LALTUTLTGAVSWLCI CCCRRKKTIKI RKKTYKTI LIDSMDEQBRMELR PKYGI KHRS
TEHNSSLMYSSSEFESDQDTLFSSRENKRGYLKGSLNGCARNGYSFGYYSKDR*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434
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820
91
1160
111
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Matches:
Conservative:
Mismatches:
Indels:
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                                       1. .4971
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                      Location/Qualifiers
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Pred. No.:
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1051 ProLysValSerMetAsnGlySerIleArgAsnGlyAlaSerPheSerTyrCysSerLys 1070
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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         2892 GTACAGAGTGGATCACCTTTCAAGGTTCTCAGAGCTGCTGCTGTGCCCCGGGAATCTGCAC
                                                                                                                                                                        AsnCysGluTrpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLeuThr
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                                                            ValGlnSerArgProProPheLysValLeuLysAlaAlaGluValAlaArgAsnLeuHis
                                                                                                                                MetArgLeuSerLysGluLysAlaAspPheLeuLeuPheLysValLeuArgValAspThr
                                                                                                                                                      2952 AAGCGGCTTTCCAAGGAGAAGAGGCCTTTCCTGCTTTTCAAGGTCTTGAGGGTAGACACA
                                                  AspllelysValGlnLysIleArgAlaHisSerAspLeuSerThrValIleValPheTyr
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                                LeuSerAsnLeuAspProGlyAsnTyrSerPheArgLeuThrValThrAspSerAspGly
                                                                                                               AlaAsnAlaGlyProAsnHisThrIleThrLeuProGlnAsnSerIleThrLeuAsnGly
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Mus musculus (nouse mouse)

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 4379)

S Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,

Alschul, S. F., Zeeberg, B., Buetow, K. H., Schemmen, C. M., Schuler, G. D.,

Alschul, S. F., Jordan, H., Morce, T., Wax, S. I., Wang, J., Haich, F.,

Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Scheetz, T. E., Brownstein, M. J. Usdin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,

Morfernan, K. J., Malle, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,

Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,

Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,

Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,

Schnerch, A., Schein, J. B., Jones, S. J. and Marra, M. A.

Generation and initial analysis of more than 15,000 full-length

Human and mouse cDNA sequences

By 2477927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov Series: IRAK Plate: 37 Row: 1 Column: 19
This clone was a selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23956263. Location/Qualifiers
                                BC028869 4379 bp mRNA linear ROD 29-JUN-2004
Mus musculus expressed sequence AU040320, mRNA (CDNA clone
MGC:28660 IMAGE:4235813), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (01-MR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="MGC:28660 IMAGE:4235813"
/tissue type="Kidney, normal. 5 month old male mouse."
/clone i="NCI CGAP_Kid14"
/lab hoet="NH10B"
/note="Vector: pCMV-SPORI6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Trisque Procurement: Jeffrey E. Green, M.D.

Tisque Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Lif. R. Consortium (LLNL)

DNA Sequencing by: The I. R. A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BAN-HGSC

Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Contact: MGC help desk
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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Strausberg, R.
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                                                                                            ArgHisValLeuValLeuProAsnAsnSerIleThrLeuAspGlySerArgSerThrAsp
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/gene="AU040320"
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evalpheTyrValGlnSerArgProProPheLysValLeuLysAlaalaGluValAlaAr :::: ::: ::: ::	3044 TĠTTGCCTTGĠĠĠATCCTG 987 rLyslleArgLysLysThr	BC014530 BC014530 Homo gapiens polycystic kidney disease 1-like, transcript variant 1, mRNA (CDNA clone MGC:11173 IMAGE:3843301), complete cds. HOMO Gapiens (human) BC014530.1 GI:45708392 MGC. Homo sapiens (human) Homo sapiens (human) BUKATYOTA; METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. RIABARYOTA; METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 4183) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Stlanser, R.D., Schaefer, G.F., Blat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L., Stapleton, M. Soares, M. B., Bonaldo, M.F., Cosavant, T.L., Stapleton, M. Soares, M. B., Bonaldo, M.F., Casavant, T.L., Stapleton, M. Soares, M. B., Bonaldo, M.F., Casavant, T.L., Stapleton, M. Soares, M. B., Bonaldo, M.F., Cosavant, S.,	Carninol, P., Parage, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., A. Gunaratne, P.H., Richards, S., McKernan, K.J., Malek, J.A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Suhterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Schnertch, A., Schein, J.W. Jones, S.J. and Marra, M.A. E Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
6 8 6 8 6 8 6 8 6	8 6 8 6 8 6 8 8	RESULT 5 BC014530 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE
		107 uThrValhlaVallysLysGluAsnAsnSerProProArgAlaArgAlaGlyGlyArgHi 177 1 1 1 1 1 1 1 1	807 uValGlnProAspProArgLysSerGlyLeuValGluLeuThrLeuGlnValGlyValGl 827

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---ThrGluHisSe 303
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    A--AATCACCTCTGGCTTCTTGAAGGAACCCCTCTCTCCAGTCATGTTTGGCTGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                       sCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuValSe 81
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GSAEVHKALITESPLTTDLABLSGGENVSVPERTQIA
GSAEVHKALITESPLTTPLABLSGGENVSVPERSELATTPSTQOKYSSERTQIA
GPOPUARSYATPTPQASFOGSTSAPYPVIRELWSAGBSVOJTLPRANDVLARYVL
BPPKGSTYTYDWQLITHPRDYSGBENGGKHSQILKLSKLIPGLYBFKVIVEGQNAHGEG
SVWTVKRPERPRARPPIAIVSPPGSISLBTTSTTAVIDGSGSTDDDKIVQYHWBELKGP
IRREKISEDTAILKLSKLIPPGAYTFSLTWVSDGATNGTTANITWKAVDYPPVANAG
PNQVITILPQNSITLFGNQSTDDHGITSYEWSLSPSSKGKVVEMQGVRTPTLQLGAMQB
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DDQK11SYLWEKTQGPDGVQLENANSSVATVTGLQVGTYVFTLTVKDERNLQSQSSVN
VIVKEEINKPPIAK1TGNVVITLPTSTAELDGSKSSDDKGIVSYLWTRDEGSPAAGEV
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HEVAAMLKSELRKQKADFLIFRALEVNTVTCQLNCSDHGHCDSFTKRCICDPFWMENF
IKVQLRDGDSNCEWSVLYVIIATFVIVVALGILSWTVICCCKRQKGKFRRKSKYKILD
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LSTDasesrcoogktofgvglrsggenhlwllectpslosclaaccodsachvewwle
Gwciqadcsrposcrafrthssnsmlvflkkfqtaddigflpeddvphllglgwnwas
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SVPNGQTPLKARSPREEIL"
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                                                                                                                  Submitted (24-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                    contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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U.S.A. 99 (26), 16899-16903 (2002)
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Conservative:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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314 rGluSerThrProSerGluLeuProIleSerProThrThrAlaProArgThrValLy9Gl 334 ::: ::: :::	ulleserHisProThrAspTyrClnGlyGlulleLysGlnGlyHisLysGlnThrLeuAs [:::	414 aFREGUESTRANDER ALTERVALIMENT AND ALTER ALGORITH AND ALGORITHM AND A	nGlyProPhelleGluGluLysThrSerValAspSerProValLeuArgleuSerAsnLe 	514 rThrThrAlaalaLeulleValAsnAsnAlaValAspTyrProProValAlaAsnAlaG1 534	574 svalvalMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAs 594	1954 TGTTALTGGCAACCTGAAACAATAACATTAGGCCTCTCAGGCAGAGGCCCAGATAAGA 2013 634 ULGUILEPheProvalGluseralaThrLeuaspGlySerSerSerSerSepaspHisGl 654 [11] [11] [11] [11] [11] [11] [11] [11]
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SAGCAGAGCACCAAAATGGTATTTTTTTTTAAAAGGA 2733 GCCATGAGGTGGCAGGGATGCTCAAGAGTGAGCTGCG 2793 HisCysAspProLeuThrLysArgCysIleCysSerHi 934 |||| :::::||| :: CTTTTGCTAAGTAGCAGCCTGATGCACTCCGAGTCAGA 3207 IlePheSerArgGluLysMetGluArgGlyAsnProLy 1052 aagataactgggaatgtggtgattacctacccacgag 2313 rgAlaGlyGlyArgHisValLeuValLeuProAsnAs 734 ArgSerThrAspAspGlnArgileValSerTyrLeuTr 754 laAlaGlyAspValIleAspGlySerAspHisSerVa 774 laAlaGluValAlaArgAsnLeuHisMetArgLeuSe 894 euphelysvalleuArgvalAspThrAlaGlyCysle 914 euAlaPheThrLeuIleValLeuThrGlyGlyPheTh 974 AGTCCTCAGATGACAAGGGAATAGTCAGCTACCTCTG SerSerThrSerThrLeuThrValAlaValLysLysGl

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117 -AGACCTGCTGTATCTTCCAGTGACCAGCAG--------
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3208 GCTGGACAGCGAT---GATGCCATCTTTACATGCCCAGACGGAGAGAAGGAAACTCCT 3264
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Screted proteins
Patent: WO 0151636-A 15 19-JUL-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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3164 AGCAGGCATCAAACAGAAAGGCCTTTTGCTAAGTAGCAGCCTGATGCACTCCCAGTCAGA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Manmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 4000)
S Hao, D. and Hooi, S.
Direct Submission
L Submitted (12-OCT-2002) Physiology, National University of
Singapore, 2 Medical Drive, Singapore 117597, Singapore
Location/Qualifiers
L. 4000
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61 sCysAspLeuSerSerCysAs 474 CTGCCAGGACTCTGCCTGCCA US-10-764-390-3 (1-1072) x AY163234 4 ProThrGlyValLeuSerSer ||| 297 CCTGTACCTGTTTTATACTTA 21 aArgLysGlnCysserGluGl :::||| 357 TGAGAGGAGGTGCCAGCAGGG uThrThrArglleMetArgVa 1 :: :: :: 417 A---AATCACCTGTGGCTTCT 81 rCysProHisLysGluAsnCy 101 rphevalleuArgProvalgi ||| |||::: 594 GTTT---TTAAAAAATTCCZ 121 uAsnArgGlySerProSerGl u***PheleuGlyLysAspTr 660 rcrgggcraggragaacrd 161 gGluLeuGluLysAspLeuLe 685 -----2.16e~120 2404.00 60.13% 47.85% 43.08% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: 628 141 41 Pred. No.: g ò g ð g ò a ò В qq g ò g δ g ò ઠે ò

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Novel human cDNA clones with function of inhibiting cancer cell
                                                                           GCTGAACTGTTCCGACCATGGCCACTGTGACTCGTTCACCAAACGCTGTATCTGTGACCC
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uLeuLysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCysIleCysSerHi
                                                                                                                                                                                                                                        934 sLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSerAsnCysGluTr
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Submitted (07-JUN-2000) National Laboratory For Oncogenes
Genes, Shanghai Cancer Institute, 25/In 2200 Xie-Tu Road,
200032, P.R. China
Location/Qualifiers
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Qin,W.X., Wan,D.F., Zhou,X.M., Zhang,P.P., Jiang,H.Q.,
Zhao,X.T. and Gu,J.R.
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Homo sapiens PP791 protein mRNA,
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YVNYTYKPERKURPPIAIUSEOFORISISLPTYSTVIDGSOSTDDDKIVOYHWEEKGP LREEKISEDTAILKLSKLVPGNYTFSLTVVDSDGATTANLTANKTVNKAVDYPPVANAG PNOVITLEONSTYLLFGROSTDDHGITSYEMSLSPSSKGRVVEMGGVRTPTLQLSAMOE GDYTYOLLTYDLTIGGQATAQVTVIVQPENNKFPQADAGPDKELTLFVDSTTLDGSSKSS

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416 141 ::: ||||||| :::||| -----AGCTTAATCAGAAGCTTCAGAAGAGAGGTAGTCCCCAGTGACGTAGTTACACC 800 627 141 u***PheLeuGlyLysAspTrpGlyLeuGluGluMetSerGluTyr***AspAspTyrAr 161 161 gGluLeuGluLysAspLeuLeuGlnProSerGlyLysGlnGluProArgGlySerAlaGl 181 181 uTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsnSerSerValGlyAs 201 201 pSerProAlaValProAlaGluThrGlnGlnAspProGluLeuHisTyrLeuAsnGluSe 221 221 rAlaSerThrProAlaProLygLeuProGluArg------SerValLeuLeuPr 237 oLeuProThrThrProSerSerGlyGluValLeuGluLysGluLysAlaSerGlnLeuGl 257 nGluGlnSerSerAsnSerSerGlyLygGluValLeuMetProSerHisSerLeuProPr 277 81 rCysProHisLysGluAsnCysGluProLysLysMetGlyProlleArgSerTyrLeuTh 101 101 rPheValLeuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMetLe 121 61 41 61 gCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuValSe 81 ProThrGlyValLeuSerSerLeuLeuLeu-----LeuValThrIleAlaGlyCys-Al 21 ::|||| :::|||| 357 TGAGAGGGAAGACACAATTTGGAGTTGGCCTGAGATCTGGGGGAGA 21 aArglysGlnCysSerGluGlyArgThrTyrSerAsnAlaValIleSerProAsnLeuGl uThrThrArg1leMetArgValSerHisThrPheProValValAspCysThrAlaAlaCy uAsnArgGlySerProSerGlyIleTrpGlyAspSerProGluAspIleArgLysAspLe 4001 521 134 319 118 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-10-764-390-3 (1-1072) x AF275679 (1-4001) 2.29e-119 2385.00 59.98% 47.71% Percent Similarity: Best Local Similarity: Alignment Scores: 237 855 685 748 121 41 417 Query Match: DB: . No. .

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qq	915 (ctrgactgcagagctgtgtgtggggggaaagaatgtaftggtgcaacctgaaatatcaga 974
č	291	oValLeuThrValThrProGlySerThrGluHisSe 303
QQ	975 (3GGTCTTGCTACTACGCCCAGCACTCAACAAGTAAAAGTTCTGAGAAAACCCAGATTGC 1034
ò	Э	31
ОР	1035	IGTCCCCCAGCCAGTGGCTCCCTCCTACAGTTATGCTACCCCTACCCCCAGGCCTCTTT 1094
ò	314	rGluSerThrProSerGluLeuProlleSerProThrThrAlaProArgThrVallysGl 334
gg	1095	
ò	334	uLeuThrValSerAlaGlyAspAsnLeuIleIleThrLeuProAspAsnGluValGluLe 354
ОР	1131	ACTGGTGGTATCTGCTGGAGAGTGTCCCAGATAACCCTGCCTAAGAATGAAGTTCAATT 1190
ò	354	uLysAlaPheValAlaProAlaProProValGluThrThrTyrAsnTyrGluTrpAsnLe 374
QQ	1191	aaargcarafircrecaagaacdacdaaaagagaaaacdaacaacdacaacdagaagaad 1250
ò	374	ulleSerHisProThrAspTyrGlnGlyGlulleLysGlnGlyHisLysGlnThrLeuAs 394
QQ	1251	GATTACTCATCCTAGAGACTACAGTGGAGAAATGGAAGGGAAACATTCCCAGATCCTCAA 1310
λ	394	
Dp	1311	ACTATCGAAGCTCACTCCAGGCCTGTATGAATTCAAAGTGATTGTAGAGGGTCAAAATGC 1370
ò	414	aPheGlyGlyGlvBheValAsnValThrValLysProAlaArgArgValAsnLeuProPr 434
Dp	1371	00000
ò	434	OValalaValValSerProGlnLeuGlnGluLeuThrLeuProLeuThrSerAlaLeuIl 454
Db	1431	
ò	454	eAspGlySerGlnSerThrAspAspThrGluIleValSerTyrHisTrpGluGluIleAs 474
qq	1491	TGATGGCAGTCAAAGCACTGATGATGATAAAATCGTTCAGTACCATTGGGAAGAACTTAA 1550
ò	474	nGlyProPhelleGluGluLysThrSerValAspSerProValLeuArgLeuSerAsnLe 494
qq	1551	GGGGCCTCTAAGAGAAGAAGATTTCTGAAGATACAGCCATATTAAAACTAAGTAAACT 1610
ò	494	uAspProGlyAsnTyrSerPheArgLeuThrValThrAspSerAspGlyAlaThrAsnSe 514
Dp	1611	GTCCCTGGGAACTACACTTTCAGCTTGATGGTAGTAGACTCTGATGGAGCTACCAACTC 1670
ò	514	rThrThrAlaAlaLeuIleValAsnAsnAlaValAspTyrProProValAlaAsnAlaGl 534
QQ	1671	TACTACTGCAAACCTGACAGTGAACAAAGCTGTGGGATTACCCCCCTGTGGCCCAACGCAGG 1730
ò	534	yProAsnHisThrIleThrLeuProGlnAsnSerlleThrLeuAsnGlyAsnGlnSerSe 554
οgo	1731	ccccaaccaagrgatcacccrgccccaaaacrccaccaccrcrrrgggaaccaggggg
ò	554	rAspAspHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySerGluGlyLysHi 574
qq	1791	TGATGATGATGACATCACCAGCTATGAGTGGTCACTCAGCCCAAGCAAAGGGAAAGT 1850
ò	574	8ValValMetGInGlyValGlnThrProfyrLeuHisLeuSerAlaMetGInGluGlyAs 594
ор	1851	GGTGGAGATGCAGGGTGTTAGAACACCAACCTTACAGCTCTCTGCGATGCAAGAAGGAGA 1910
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                                                                                                                                       303 ATTGATGGCAGTCAAAGCACTGATGATGATAAAATCGTTCAGTACCATTGGGAAGAACTT
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                                  AlaPheGlyGluGlyPheValAsnValThrValLysProAlaArgArgValAsnLeuPro
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                                                17-JAN-2003
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1 (Dases 1 to 2796)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishil,S., Sujiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 15398 09-UUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA,AI WAKAMATSU,
KEIICHI NAGAI,TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 LeulysalaphevalalaproalaproprovalGluThrThrTyrAsnTyrGluTrpAsn 373
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Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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JP 2002191363-A/15398
09-JUL-2002
28-JUL-2000 JP 2000280990
SPITO, OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI SAITO,
                                                                                                                           GlyAsnProLysValSerMetAsnGlySerIleArgAsnGly 1062
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427
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// db_xref="taxon:9606"
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Primer for synthesizing
BD160555
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JP 2002191363-A/15398.
Homo sapiens (human)
Homo sapiens
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SITLESKUVPGNYTPSLITVUSBOGATNSTTANLTVNKAVDYPPVANGGBNOVITLEON
SITLEGOGATDGHGITSYEMSLSSSKGKVVEMÇGKRTPTLQLSAMGEGDYTYQLIVT
DITGQOATAQVYUVQPENNKEPPQADGEDTLLFUPVDSTTLDGSKSSDDQKISYLW
PIAKITGNVVITLPTSTABLDGSKSSDDKGIVSYLWTRDEGSPAGEVLAHSDHFFIL
PISKITGNVVITLPTSTABLDGSKSSDDKGIVSYLWTRDEGSPAGEVLAHSDHFFIL
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ILRKQKADPLIFRALEVNTVTCQLNCSDHGHCDSFTKRCICDFFWMENFIKVQLRDGDS
NCBWSTLYVIIATFVIVVALGILSWTVICCCKRQKGKRKKKKKKILLDATDQESLELK
PTSRAGIKQKGLLLSSSLWHSESELDSDDAIFTWPDNEEKGKLLHGQNGSVPNGQTPLK
ARSPREEIL"
          Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 18736 07-FEB-2001; Research Association for Bittechnology (JP) Location/Qualifiers
                                                                                                                                                                                                  /proteIn_id="CAE92130.1"
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Mismatches:
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                                                                                                             /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                   ABPSerGlnGlyAlaSerAspThrAspThrAlaThrValGluValGlnProAspProArg
                                                                                                                                                            CCTTTTGGATGGAGAATTTCATCAAGGTGCAGCTGAGGGATGGAGACAGCAACTGTGAG
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                           774 ValAlaLeuGlnLeuThrAsnLeuValGluGlyValTyrThrPheHisLeuArgValThr
                                          CTATCCTTTTCTTTCAAACCTGGTTGAGGGAACCTACACTTTTCACCTGAAAGTGACC
                                                                                                                                             LysSerGlyLeuValGluLeuThrLeuGlnValGlyValGlyGlnLeuThrGluGlnArg
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I sogai,T. and Otsuki,T.

Direct Submission

Submitted (123-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mall;GenomicsGhri.co.jp, Tel:81-438-52-3976, Pax:81-438-52-3986)
NEDO human CDNA sequencing project supported by Ministry of International Trade and Industry of Japan, CDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, S - & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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GMFIRQIGVLLGVLDSDIIVQKIQPYTEQSTRAVFFYQNEPPHQIFKGHEVAAMLKSB
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PYSRAGILKQKGLLLSSSLMHSESELDSDDAIFTWPDREKGKLLHGQNGSVPNGQTPLK
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/ DECOLETI 16="BAB14874.1"

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Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shiraj, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakal, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs
                                                                                                                                                                                                                                                           Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Magai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishiis, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, R., Nagahari, K., Masuho, Y., Minomiya, K. and Iwayanagi, T., Malo, human CDNA sequencing project
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precursor cells after 2-weeks retinoic acid (RA)
induction."
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ThrValLysAspGlnGlnGlyLeuSerThrSerThrLeuThrValAlaValLysLys 713

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Similarity:

Best Local

Query Match: DB:

Percent Similarity:

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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uoduellano, N.A., Peters, G.J., Morkernan, K.J., Malek, J.A., Guaratane, P.J., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Roud, A.C., Shevchenko, Y., Butterfield, S., Garcia, A.M., Green, E.D., Dickson, M.C., Roditjuez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Green, E.D., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 52 Row: c Column: 4.
                                              LUCALD / 2
HOMO Sapiens polycystic kidney disease 1-like, mRNA (cDNA clone IMAGE:4446786), partial cds.
                                                                                                                                                                                                                                                                      Euteleostomi;
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Submitted (06-707-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, PH., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, F.Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone_lib="NIH MGC_89"
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Contact: MGC help desk
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                                                                             ValGlnLysIleArgAlaHisSerAspLeuSerThrValIleValPheTyrValGlnSer
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Conservative:
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Indels:
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Prediction of the coding sequences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 8 (2), 85-95 (2001)
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                                                                                          GTGATCTGTTGTAAGAGGCAAAAA---GGAAAAACCCAAGAGAAAAGCAAGTACAAG 1859
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                                                                     PhelyryalThrvalLeuAlaPheThrLeuIlevalLeuThrGlyGlyPheThrTrpLeu 976
                                                                                                                                             CysileCysCysCysLysArgGlnLysArgThrLysIleArgLysLysThrLysTyrThr 996
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens mRNA for KIAA1837 protein, partial cds.
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Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
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Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	t Scores: .: Similarity: al Similarity: tch:	8e-99 2005.50 74.92* 61.59* 35.94*	Length: Marches: Conservative: Mismatches: Indels: Gaps:	4423 388 84 155 3
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ò	383 GlyGluIle	GlyGlulleLysGlnGlyHis	sbysGlnThrLeuAsnLeuSerGlnL	leuSerGlnLeuSerValGly 401
QQ	22 GGATGAGTA	::: ATGGAAGGGAAACAT	TCCCAGATCCTCAAAC	::: ::
à	402 LeuTyrval	PheLysValThrVal	SerSerGluAsnAlaP	LeuTyrValPheLysValThrValSerSerGluAsnAlaPheGlyGluGlyPheValAsn 421
QQ Q	82 CTGTATGAA	TTCAAAGTGATTGTA	GAGGGTCAAAATGCCC	CIGTATGAATTCAAAGTGATTGTAGAGGGTCAAAATGCCCATGGGGAAGGCTATGTGAAC 141
à	422 ValThrVal	Lysproalaargarg	ValAsnLeuProProV	ValThrValLysproAlaArgArgValAsnLeuProProValAlaValValSerProGln 441
Db	142 GTGACAGTC	AAGCCAGAGCCCCGT	AAGAATCGGCCCCCCA	GTGACAGTCAAGCCCCGTAAGAATCGGCCCCCCATTGCTATTGTGTCACCTCAG 201
Ġ	442 LeuGlnGlu	LeuThrLeuProLeu	ThrSerAlaLeuIleA	LeuGlnGluLeuThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThrAsp 461
Dp	202 TTCCAGGAG	arcretteccaace	ACTICTACAGECATIG	TTCCAGGAGATCTCTTTGCCAACCACTTCTACAGTCATTGATGGCAGTCAAAGCACTGAT 261
ò	462 AspThrGlu	IleValSerTyrHis	TrpGluGluIleAsnG	AspThrGluleValSerTyrHisTrpGluGluleAsnGlyProPheIleGluGluLys 481
Dp	262 GATGATAAA	ATCGTTCAGTACCAT	TGGGAAGAACTTAAGG	
Ġ	482 ThrSerVal	AspSerProValleu	ArgleuSerAsnLeuA	erValAspSerProValLeuArgLeuSerAsnLeuAspProGlyAsnTyrSerPhe 501
qq	322 ATTTCTGAA	GATACAGCCATATTA	AAACTAAGTAAACTCG	ATTTCTGAAGATACAGCCATATTAAAACTAAGTAAACTCGTCCCTGGGAACTACACTTTC 381
ò	502 ArgLeuThr	ArgLeuThrValThrAspSerAspGlyAlaThrAsnS	GlyAlaThrAsnSerT	erThrThrAlaAlaLeuIleVal 521
Db	382 AGCTTGACT	GTAGTAGACTCTGAT	GGAGCTACCAACTCTA	AGCTTGACTGTAGACTCTGATGAGGAGCTACCAACTCTACTACTGCAAACCTGACAGTG 441
ò	522 AsnAsnAla	ValAspTyrProPro	roValAlaAsnAlaGlyP	BnAsnalavalAspTyrProProValAlaAsnAlaGlyProAsnHisThrIleThrLeu 541
QQ	442 AACAAAGCT	GTGGATTACCCCCCT	GTGGCCAACGCAGGCC	AACAAAGCTGTGGATTACCCCCCTGTGGCCCAACGCAGCCCCCAACCAA
ò	542 ProGlnAsn	SerileThrLeuAsn	GlyAsnGlnSerSerA	ProGlnAsnSerlleThrLeuAsnGlyAsnGlnSerSerAspAspHisGlnIleValLeu 561
g	502 CCCCAAAAC	TCCATCACCCTCTTT	GGGAACCAGAGCACTG	CCCCAAAACTCCATCACCCTCTTTGGGAACCAGAGCACTGATGATCATGGCATCACCAGC 561
ò	562 TyrGluTrp	SerLeuGlyProGly	SerGluGlyLysHisV	TyrGluTrpSerLeuGlyProGlySerGluGlyLyBHisValValMetGlnGlyValGln 581
qq	562 TATGAGTGG	TCACTCAGCCCAAGC	AGCAAAGGGAAAGTGG	srggargeaggergrraga 621
ò	582 ThrProTyr	LeuHisLeuSerAlal	MetGlnGluGlyAspT	ThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAspTyrThrPheGlnLeuLysVal 601
qq	622 ACACCAACC	TTACAGCTCTCTGCG	ATGCAAGAAGGAGACT	ACACCAACCTTACAGCTCTCTGCGATGCAAGAAGGAGACTACTTACCAGCTCACAGTG 681
à	602 ThraspSer	SerArgGlnGlnSer	ThrAla***ValThrV	ThrAspSerSerArgGlnGlnSerThrAla***ValThrValIleValGlnProGluAsn 621
Ωp	682 ACTGACACA	ATAGGACAGCAGGCC	Actectcaagreacte	FTTATTGTGCAACCTGAAAC 741
ò	622 AsnArgPro	ProValAlaValAla	GlyProAspLysGluL	AsnArgProProValAlaValAlaGlyProAspLysGluLeuIlePheProValGluSer 641

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CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
                                                                                              2501 bp DNA linear proteins and polynucleotides encoding them.
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Secreted proteins and polynucleotides encoding them Serreted proteins and polynucleotides encoding them CENETICS INSTITUTE INC
PN JP 2001514520-A/8
PD 11-SEP-2001
PP 09-MAR-1998 JP 1998539683
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, I
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                        AspGluGlnGluArgMetGluLeuArgPro 1011
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                                                                                                 ThrGlyLeuGlnValGlyThrTyrHisPheArgLeuThrValLysAspGlnGlnGlyLeu
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922 ACTGGGCTGCAAGTGGGGACCTATGTGTTCACCTTGACTGTCAAAGATGAGAGGAACCTG
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ThrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThrAla * * ValThrVal
                                                                   ACCCTTCTGTGGATAGCACAACCCTGGATGGCAGCAAGAGCTCAGATGATCAGAAAATT
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                                       956 IlePheTyrValThrValLeuAlaPheThrLeuIleValLeuThrGlyGlyPheThrTrp
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US-10-764-390-3 5580 1 MAPPIGVLSSLLLLVTIAGC.....VSMNGSIRNGASFSYCSKDR 1072 score: Sequence: Title: Perfect

Scoring table:

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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1: geneseqpl9802: geneseqpl980geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:*geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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8.8 8.3	7.2	5. 9	4.9	4.2	4.0	4.0	4.0	4.0	3.9	3.8	3.8	3.8	3.8	3.7	3.7	3.6	3.6	3.6
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ALIGNMENTS

RESULT 1

mitochondrial; human; screening assay; diabetes mellitus; huntington's disease; osteoarthritis; Lubber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; myoclonic epilepy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic. Human heat mitochondrial protein as a therapeutic target SeqID1622. ADJ69816 standard; protein; 1072 AA. 06-MAY-2004 (first entry) ADJ69816; ADJ6981

sapiens Homo

WO2003087768-A2

23-OCT-2003

04-APR-2003; 2003WO-US010870.

12-APR-2002; 2002US-0372843P. 17-JUN-2002; 2002US-0389987P. 20-SEP-2002; 2002US-0412418P.

(MITO-) MITOKOR. (BUCK-) BUCK INST AGE RES.

Glenn GM; Gibson BW, Taylor SW, Zhang B, Fahy ED, Warnock DE; Ghosh SS,

WPI; 2003-845369/78.

Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.

Claim 1; SEQ ID NO 1622; 180pp; English.

This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for

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identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with alered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, antiantonylsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
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120 180 120 240 240 300 360 420 420 480 480 540 540 600 900 99 99 720 720 780 780 840 9 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKWGPIRSYLTFVLRPVQRPAQLLDYGDWM LNRGSPSGIWGDSPEDIRKDLTFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSA TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP NYTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT LPQNSITLINGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK VIDSSRQOSTAVVIVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN LVEGYYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT L.P.QNS.ITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK VTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW EHVRGPSAVEMENI DKA I ATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR 61 61 121 121 181 181 241 301 361 361 421 421 481 481 541 541 601 661 661 721 781 301 601

The present invention describes a 254Plb6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254Plb6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists essentially of, or consists of a peptide of eight, nine, ten, or consists essentially of, or consists of a peptide of eight, nine, ten, or cleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID No.3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or a protein clattical to an entire amino acid sequence of Pl; (2) a polymucleotide clattical to an entire amino acid sequence of Pl; (2) a polymucleotide that is a full complement of the polymucleotide described above, (4) centaring a mammalian immune response directed to the protein of Pl; (5) detecting, in a sample, the presence of a 254Plb6B-related protein or

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SEQ ID NO 11; 345pp; English.

Example 1;

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961 VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKKTKYTILDNMDEQERMELRPKYGIKHRST 1020
                                                                                                                 VLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNWDEQERMELRPKYGIKHRST 1020
                                                                                           960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting
781 LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ
                                                                                LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT
                                    LAVLLIVILDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF
                       LAVLLNVLDSDI KVQKI RAHSDLSTVI VFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF
                                                                                                                                                                                                                                                                                                                                          254P1D6B; small interfering RNA; siRNA; immune response;
254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
254P1D6B v.5; chromosome 6.
                                                                                                                                                                             EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072
                                                                                                                                                                EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                     Human 254PlD6B v.5 protein SEQ ID NO:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jakobovits A,
                                                                                                                                                                                                                                                 Z
                                                                                                                                                                                                                                               ADR00600 standard; protein; 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JAN-2004; 2004WO-US001965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-2003; 2003US-0442526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perez-Villar JJ, Faris M;
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-580991/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein or correspor
and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004067716-A2.
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                              04-NOV-2004
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The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to 254PID6B protein, open reading frame (ORF) sequence which encodes the 254PID6B protein, or corresponds to aubsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, S or 7 ADRO0592, ADRO0594 or ADRO0596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein Human nov FITC labe FITC labe FAM label Human 254 Human 254 Human 254 Human 254 Human 254 Conjugate Peptide e Human nov New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer. Peptide e Gal N-a DIC. Integrin Human Human Human 254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.5; chromosome 6. Add 25603 Add 2607 Add 2607 Add 25439 Add 10694 Add 100725 Add 100725 Add 100725 Add 100725 Add 10072 Add 10072 Add 2007079 Add 2007079 Add 2007079 Add 2007079 Add 2007079 Add 2007079 Add 2007079 Add 2007079 Add 2007079 3 g Challita-Eid PM, Example 13; SEQ ID NO 268; 345pp; English. ALIGNMENTS Human 254PlD6B v.5 peptide SEQ ID NO:268 Jakobovits A, ADR00810 AAP81554 ADI80581 AAB25607 ADA27079 ADE86611 ABU07534 ADE25869

Peptide e Human nov

ADR00641 AAB25609 ADA27081 ADE86613

Query Match

Score

Result Š. 1158 1101 999 92 90 94 83 73

gen

Human

Human Human Human

Add 2509 B Add 2708 B Add 2708 B Add 2727 B Add 2727 B Add 2728 B

Human Human

ADR00829 ADR00639 ADR00675

ADR00814

Integrin

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generating a mammalian immune response directed to the protein of Pi; (5) detecting, in a sample, the presence of a 254Plb6B-related protein or a 254Plb6B-related protein or a 254Plb6B-related polynucleotide; (6) a composition that modulates the status of a cell that expresses a protein of Pi; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a
   98, or 99% homologous or
                                                                                                                                                                                                                                                                                                                                                  hybridoma that produces the antibody! (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254P1D6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254P1D6B v. 5 peptide, which is used in the exemplification of the present invention. The human 254P1D6B gene is located on chromosome 6p22.
                          identical to an entire amino acid sequence of P1; (2) a polymuclectide that encodes the protein; (3) a composition comprising a polymuclectide that is a full complement of the polymuclectide described above; (4)
      95, 96, 97,
   is at least 90, 91, 92, 93, 94,
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Sequence 29 AA;

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Gaps
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2.8%; Score 158; DB 8; Length 29; 96.6%; Pred. No. 0.00021; ive 0; Mismatches 1; Indels
                                                           128 GIWGDSPEDIRKDLXFLGKDWGLEEMSEY 156
                                                                           1 GIWGDSPEDIRKDLTFLGKDWGLEEMSEY 29
             Local Similarity 96.6
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Matches
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ADR00851 standard; peptide; 29 AA.
        (first entry)
        04-NOV-2004
     ADR00851;
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Human 254PlD6B v.2 peptide SEQ ID NO:262.

254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.2; chromosome 6.

Homo sapiens.

WO2004067716-A2

12-AUG-2004

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P

(AGEN-) AGENSYS INC.

3 g Challita-Eid PM, Jakobovits A, Perez-Villar JJ, Faris M; Kanner SB, Raitano AB, WPI; 2004-580991/56. New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting

Example 13; SEQ ID NO 262; 345pp; English.

and treating cancer.

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that compresses a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PID6B protein, or corresponds to a subsequence of the ORF, where the

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consists essentially of, or consists of a peptide of eight, nine, ten, or consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ 1D NO:3, 5 or 7 AbR00592, AbR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that each see 191, 91, 92, 93, 94, 95, 96, 97, 98, or 99* homologous or identical to an entire amino acid sequence of P1; (2) a polynuclectide that encodes the protein; (3) a composition comprising a polynuclectide contains a full complement of the polynuclectide described above; (4) contains a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254P1D6B-related protein or a C2 54P1D6B-related polynuclectide; (6) a composition that modulates the capture of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human composition that comprises the antibody; (17) a pharmaceutical confidence to a cell that expresses the protein of P1; and confidence to a confidence of a 254P1D6B related protoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and c(12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1; and c(12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254P1D6B has cytostatic activity, and can be composition and detecting cancer. The present sequence represents a chuman 254P1D6B v.2 peptide, which is used in the exemplification of the composition. The human 254P1D6B gene is located on chromosome 6p22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.2; chromosome 6.
  double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.7%; Score 152; DB 8; Length 29; 96.6%; Pred. No. 0.00059; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Challita-Bid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 FLGKDWGLEEMSEYXDDYRELEKDLLQPS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLGKDWGLEEMSEYADDYRELEKDLLQPS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 254PID6B v.2 peptide SEQ ID NO:261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jakobovits A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR00850 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-2004; 2004WO-US001965.
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Perez-Villar JJ, Faris M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004067716-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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ADR00850
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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the cast be useful open reading frame (ORF) sequence which encodes the cast be useful or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists essentially of, or consists of a peptide of eight, nine, ten, or cleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO.3, 5 or 7 ADRO0529, ADRO0559, or ADRO0596, or a peptide included in any of the 42 lists of peptides given in the specification, or a protein cany of the 42 lists of peptides, 99, 96, 97, 98, or 99; homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99; homologous or clentical to an entire amino acid sequence of P1; (2) a polymuclectide that is a full complement of the polymuclectide described above; (4) detecting in a sample, the presence of a 254P1D6B-related protein or a 254P1D6B-related polymuclectide; (6) a composition that modulates the capture of a call that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or the fragment, which is monoclonal; the antibody or the fragment, which is monoclonal; the antibody or a protein or a composition animal that produces the antibody; (10) a pharmaceutical animal transgent or the protein or a composition that comprises the composition described above in a human cuit dose form; (8) an antibody or the fragment, which is monoclonal; the antibody or the fragment, which is monoclonal; the protein or a composition animal that produces the monoclonal; the protein or a composition animal that produces the monoclonal; the protein or a composition animal that produces the composition or a composition animal that produces the composition or a composition animal that produces the composition or a composition ani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hybridoma that produces the antibody, (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1, and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254P106B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254P106B v.2 peptide, which is used in the exemplification of the present invention. The human 254P106B gene is located on chromosome 6p22.
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254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
254P1D6B v.5; chromosome 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 101; DB 94.7%; Pred. No. 1.6; ive 0; Mismatches
Example 13; SEQ ID NO 261; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 254PlD6B v.5 peptide SEQ ID NO:267.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR00856 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 WGLEEMSEYXDDYRELEKD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-2004; 2004WO-US001965.
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Perez-Villar JJ, Faris M;
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nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AGEN-) AGENSYS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 AA;
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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the case the nucleotides in case of the ore sequence of the ORF, where the 254P1D6B protein, or corresponds to a subsequence of the ORF, where the cability of the 20, 21, 22, 23, 24, or 25 contiguous consists essentially of consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID NO:3, 5 or 7 ABN06929, ABN06934 or ABN06956), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of a camposition that modulates the captures of a 254P1D6B-related protein or a 254P1D6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition deave in a human current or should be an antibody or its fragment, which is monoclonal; (9) a non-human transgance animal that produces the antibody; (10) a non-human transgance animal that produces the antibody; (10) a non-human transgance animal that produces the antibody; (10) a non-human transgance animal that produces the antibody; (10) a non-human transgance animal that produces the antibody; (10) a non-human transgance animal that produces the antibody; (10) a non-human transgance animal that produces the antibody; (10) a non-human transgance animal that produces the antibody; (10) a non-human transgance animal that produces the antibody; (10) a non-human transgance animal that produces the animal animal transgance animal that produces the animal animal transgance animal that produces the animal animal transgance animal transgance animal that produces the anima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hybridoma that produces the antibody; (11) delivering a cyctoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cycostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254PlD6B v. 5 peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                   New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
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254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 99; DB 8;
94.7%; Pred. No. 2.3;
tive 0; Mismatches
                                                                                                                                                      Example 13; SEQ ID NO 267; 345pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR00632 standard; peptide; 16 AA.
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les 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 AA;
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Matches
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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254P1D6B protein, or corresponds to a subsequence of the occess the consists acid open reading frame (ORF) sequence which encodes the consists essentially or corresponds to a subsequence of the ORF, where the consists essentially of, or consists (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 [Pl., see SEQ ID NO.3, 5 or 7 ADRO0592, ADR00594 or ADR00596), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98 homologous or contrict that is a full complement of the polynucleotide described above; (4) contact is a full complement of the polynucleotide described above; (4) contact is a full complement of the polynucleotide described above; (4) composition that modulates the composition that modulates the composition that comprises the composition described above in a human comprise of a call that expresses a protein of Pl; (7) a pharmaceutical comprises the antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent confidence form; (8) an antibody or its fragment, which is monoclonal; (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of Pl; 254P1D6B has cytostatic activity, and call that express the protein of Pl; 254P1D6B has cytostatic activity, and call that express the protein of Pl; 254P1D6B has cytostatic activity, and call that express the protein of Pl; 254P1D6B has cytostatic activity, and call that express the protein of Pl; 254P1D6B has cytostatic activity, and call that express the protein of Pl; 254P1D6B has cytostatic activity, and call that express the protein of Pl;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                             New 254P1D6B siRNA composition comprising a double stranded siRNA that
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                                                                                                                          Challita-Eid PM,
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                                                                                                                          Jakobovits A,
                                                                                                                          Kanner SB, Raitano AB, J
Perez-Villar JJ, Faris M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and treating cancer.
                                                                                                                                                                                                                                                                                                        WPI; 2004-580991/56.
(AGEN-) AGENSYS INC
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New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting

Example 13; SEQ ID NO 266; 345pp; English.

and treating cancer.

Ge ≅;

Jakobovits A, Challita-Eid PM,

Kanner SB, Raitano AB, Ja Perez-Villar JJ, Faris M;

(AGEN-) AGENSYS INC.

WPI; 2004-580991/56.

23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P.

12-AUG-2004.

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ADR00849;
                                                                                                                 Query Match
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                            ADR00849
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                                     ö
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                             254PID6B; small interfering RNA; siRNA; immune response;
254PID6B-related protein; cytostatic; gene therapy; cancer; human;
254PID6B v.5; chromosome 6.
                                     ö
 1.6%; Score 92; DB 8; Length 16;
                                     0; Indels
                   5.6;
Query Match 1.6%; Score 92; DB Best Local Similarity 100.0%; Pred. No. 5.6 Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                          Human 254P1D6B v.5 peptide SEQ ID NO:266.
                                                                                                                                                                                                            ADR00855 standard; peptide; 17 AA.
                                                                           522 NNAVDYPPVANAGPNH 537
                                                                                                 04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                  ADR00855;
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RESULT 6

셤 ठ

WO2004067716-A2

Ното варіелв.

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The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PID6B protein, or corresponds to subsequence of the ORF, where the couples stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous concludes in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or cleven contiguous amino acids of a protein of figure 2 (PI, see SEQ ID CN 03, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein CC that is at least 90, 91, 92, 94, 95, 96, 97, 98, or 99‡ homologous or identical to an entire amino acid sequence of PI; (2) a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide confidential in manner response directed to the protein or a confirmation in a sample, the presence of a 254PID6B-related protein or a 254PID6B-related polymucleotide; (6) a composition that modulates the composition that modulates the composition that modulates the composition described above in a human cc unit dose form; (8) an antibody or its fragment, which is monoclonal; confirmathat produces the antibody or its fragment, which is monoclonal; confirmathat produces the antibody or its fragment, which is manner and an antibody or its fragment, which is manner and an antibody or its fragment, which is manner and an antibody or its fragment, which is manner and an antibody or its fragment, which is manner and an antibody or its fragment, which is manner and an antibody or its fragment, which is manner and an antibody or its fragment, which is manner and an antibody or its fragment, which is manner and an antibody or its fragment, which is manner and an antibody or its fragment, and an antibody or its fragment and an antibody or its fragment and an antibody or its fragment and an antibody or its fragm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hybridoma that produces the antibody; (11) delivering a cycotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and class growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254PlD6B v. 5 peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
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254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·,
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Pred. No. 8.7;
0; Mismatches
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94.1%; Pred
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 PEDIRKDLXFLGKDWGL 150
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les 16; Conserv
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) as useful in gene therapy techniques to restore normal cativity of (II) and to the teat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful in medical imaging of sincolving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostic seaponsible for genefic dissorders or other traits to assess blodiversity are polypeptide of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                         Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5%; Score 83; DB 4; Length 19; 100.0%; Pred. No. 34;
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                                                      Novel human diagnostic protein #22057.
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100.08;
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                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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18-FEB-2002 (first entry)
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nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                            WO200175067-A2.
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                                                                                                                                                                                           Homo sapiens
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the couposition that caid open reading frame (ORF) sequence which encodes the couple stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PlD6B-related polynucleotide; (6) a composition that modulates the captures the composition described above in a human cut dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgent to a call that expresses a protein of P1; (7) a pharmaceutical correct or a diagnostic agent to a cell that expresses the protein of P1; (10) a non-human transgent to a composition and methods are useful (12) inhibiting growth, reproduces the antibody; (11) delivering a cyclotoxic agent or a diagnostic agent to a composition or survival of cancer cells that expresses the protein of P1; or a diagnostic agent to a composition or survival of cancer cells that expresses the protein of P1; and C12) inhibiting growth, reproducing or every measure sequence represents a human 254PlD6B v.2 peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
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                                                                                                                                                                                                                                                                                                                                                                               Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; SEQ ID NO 260; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Jakobovits A,
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                                                                                                                                                                                                               23-JAN-2004; 2004WO-US001965
                                                                                                                                                                                                                                                                     24-JAN-2003; 2003US-0442526P
                                                                                                                                                                                                                                                                                                                                                                                                           Perez-Villar JJ, Faris M;
254PlD6B v.2; chromosome
                                                                                                                                                                                                                                                                                                                                                                                  Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-580991/56.
                                                                                                                                                                                                                                                                                                                         (AGEN-) AGENSYS INC.
                                                                                                         WO2004067716-A2
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                                                        Homo sapiens.
                                                                                                                                                            12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                  Kanner SB,
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Gaps

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RESULT 8 ABG22066

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254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human;

Human 254P1D6B peptide SEQ ID NO:138.

(first entry)

04-NOV-2004

ADR00727;

ġ.

ADR00727 standard; peptide; 9

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID ONC), So T ARROSSY, ARROSSY, ARROSSY, or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein cany of the 42 lists of peptides, given in the specification, or a protein cany of the 42 lists of peptides, given in the specification, or a protein cany of the 42 lists of peptides, given in the specification, or a protein cany of the protein of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) a cangosition and anomalian immune response directed to the protein or a 24F1D6B-related protein or a 254F1D6B-related protein or a 254F1D6B-related polynucleotide; (6) a composition that modulates the composition that modulates the composition that comprises the composition does form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the animal and animal and animal and animal and animal and animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
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                                                                                                                                                                254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.3; chromosome 6.
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                                                                                                     254PlD6B; small interfering RNA; siRNA; immune response;
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Human 254PlD6B v.3 peptide SEQ ID NO:265.
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Best Local Similarity 100.
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-580991/56.
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                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kanner SB,
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New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting

Example 9; SEQ ID NO 138; 345pp; English.

and treating cancer.

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Challita-Eid PM,

Jakobovits A,

Kanner SB, Raitano AB, Perez-Villar JJ, Faris

(AGEN-) AGENSYS INC.

WPI; 2004-580991/56.

23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P

WO2004067716-A2

12-AUG-2004.

chromosome 6. Homo sapiens.

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The present interaction that comprises a 237-fine breath interacting the composition that comprises a double stranded shrNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the cube nucleotides protein, or corresponds to a subsequence of the ORF, where the double stranded shrNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a perotein of figure 2 (Pt, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98 homologous or that encodes the protein; of a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) composition in a sample, the presence of a 254PID6B-related protein or a 254PID6B-related polynucleotide described above; (4) composition that modulates the composition described above in a human curit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgent can antibody or its fragment, which is monoclonal; (12) inhibiting growth, reproduction or antibody; (10) a non-human transgent to a cell that expresses the antibody; (10) a continuity of cancer cells that expresses the protein or survival of cancer cells that expresses the protein or survival of cancer cells that expresses the protein or survival of cancer cells that expresses the protein or survival of cancer cells that expresses the protein or survival or cancer cells that expresses the protein or survival or cancer cells that expresses the protein or survival or cancer cells that expresses the protein or survival or cancer cells that expresses and mathematical and mathematical expresses the protein or survival or cancer cells that expresses the protein or survival or cancer cells that expresses and mathematical and mathematical and mathematical and mathematical and mathematical and mathematical and mathematical and mathematical and mathematical and mathematical and mathemat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes a 254P1D6B small interfering RNA (siRNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
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946 WDGESNCEW 954

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Gaps

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Indels

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RESULT 10 ADR00727

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The invention provides a method of diagnosis of tauopathies in an individual that comprises determining the ratio of phospho-tau (181)/
c total tau. Tau and phospho tau are useful as neurological markers for the manufacture of a diagnostic kit for the diagnosis of a tauopathy and/or the differential diagnostic kit for the diagnosis of a tauopathy and or the differential diagnostic form an immunological complex with monoclonal antibody HT7 and MAA AT270 comprising at least the minimal epitope of HT7 or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy or for the differential diagnosis of a tauopathy versus a non and/or for the differential diagnosis of a tauopathy versus a non caupathy. The kit is useful for the diagnosis of Alzheimer's disease, pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal dementia and/or Frontotemporal dementia and/or for neurotoxicity in patients with leukemia. The disease, stroke and/or neurotoxicity in patients with leukemia. The for determining the effectiveness of a treatment. The present sequence represents a phospho-peptide binding to MADS HT7 and AT270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the ratio of phospho-tau / total tau is useful for diagnosing a tauopathy i.e. Alzheimer's disease or Pick's disease, versus a non tauopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 61.5; DB 4; Length 34;
29.6%; Pred. No. 3.2e+03;
ive 6; Mismatches 7; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tauopathy; phospho-tau (181); neurological marker; monoclonal antil
HT7; AT270; nootropic; neuroprotective; cerobroprotective; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibodies HT7 and AT270 binding phospho-peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                 AAB85615 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vanderstichele H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 40; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JAN-2000; 2000EP-00870008.
27-JAN-2000; 2000US-0178391P.
22-NOV-2000; 2000EP-00870280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JAN-2001; 2001WO-EP000560.
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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WPI; 2001-476242/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200155725-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vanmechelen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-2001
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                                                                                                                                                                                                                                                                                                                   AAB85615;
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                                                                                                                                                       RESULT 11
                                                                                                                                                                                                AAB8561
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The present invention describes a method for the differential diagnosis of an individual suffering from Alzheimer's disease versus an individual suffering from neurological disease involves using phospho-tau (1) as a neurological marker. Also described are: (1) a diagnostic kit for use in the differential diagnosis of an individual suffering from Alzheimer's disease versus an individual suffering from another neurological disease; and (2) use of an antibody that specifically recognises (1) for the manufacture of the diagnostic kit. (1) has neuroprotective and nootropic activities, and can be used as a neurological marker in the differential clasmosis and in the manufacture of a diagnostic kit for the differential clasmosis of an individual suffering from Alzheimer's disease versus an individual suffering from another neurological disease such as dementics with Lewy bodies, Parkinson's disease without dementia, multi-system arrophy and/or progressive supranuclear palsy; and for screening or monitoring the effect on an individual of compounds which prevent on an individual of compounds which prevent or an individual compounds which prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individual prevent or an individua
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                                                                                                                                                                                                                                       Cerebrospinal fluid; CSF; beta amyloid; differential diagnosis; neurological disease; Alzheimer's disease; neuroprotective; nootropic; dementic; Parkinson's disease; dementia; multi-system atrophy; progressive supranuclear palsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for the differential diagnosis of an individual suffering from Alzheimer's disease versus an individual suffering from another neurological disease involves use of phospho-tau as a neurological
                                                                                                                                                                                         Cerebrospinal fluid (CSF)-beta-amyloid synthetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "phosphorylated threonine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vanmechelen E, Vanderstichele H, Hulstaert F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "acetylated"
                          ABB05625 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 18; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2001; 2001WO-EP007029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000EP-00870151.
18-JUL-2000; 2000US-0218907P.
                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-171654/22.
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Modified-site
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                                                                                                                                     23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                 ABB05625;
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ABB05625
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Local Similarity 29.6 nes 21; Conservative

Matches

236 LPLPTTPSSGE 246

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RESULT 14
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                                                                            176 PRGSAEYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related polymucleotide; (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New 254PID6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PID6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                      1 PRGAAP-----PGQKGQANAT----RIPAKT------PPAPKTP---- 29
                                                     Gaps
                                                                                                                                                                                                                                                                                                                               254PlD6B; small interfering RNA; siRNA; immune response;
254PlD6B-related protein; cytostatic; gene therapy; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                    7; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                           Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Challita-Eid PM,
                          Score 61.5; DB 5;
Pred. No. 3.2e+03;
                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; SEQ ID NO 41; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jakobovits A,
                                                                                                                                                                                                                                                                                                      Human 254P1D6B peptide SEQ ID NO:41.
                                                                                                                                                                                                                           ADR00630 standard; peptide; 12 AA.
                           1.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JAN-2004; 2004WO-US001965.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kanner SB, Raitano AB, J
Perez-Villar JJ, Faris M;
                                                                                                                                                                                                                                                                              (first entry)
                        Query Match
Best Local Similarity 29.6
Matches 21; Conservative
                                                                                                                                236 LPLPTTPSSGE 246
                                                                                                                                                           -----PSSGE 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                             WO2004067716-A2.
 Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            chromosome 6.
                                                                                                                                                                                                                                                                              04-NOV-2004
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                        hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pi; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of Pi. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254PID6B; small interfering RNA; siRNA; immune response;
254PID6B-related protein; cytostatic; gene therapy; cancer; human;
a non-human transgenic animal that produces the antibody; (10) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
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. 7.8e+02;
1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 8
Pred. No. 7.8e+
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 254P1D6B peptide SEQ ID NO:137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR00726 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-2004; 2004WO-US001965.
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                                                                                                                                                                                                                                                                                                                                                                                                        1.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.7
Matches 11, Conservative
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EEMSEYSDDYRE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AGEN-) AGENSYS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perez-Villar JJ,
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                                                                                                                                                                                                                                                                                                                                         Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pi; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of Pi. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                        detecting, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related protein or a 254PlD6B-related polynucleotide; (6) a composition that modulates the status of a cell that expresses a protein of Pl; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a
9
generating a mammalian immune response directed to the protein of P1;
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Sequence 9 AA;

Gaps ö 0; Indels 1.1%; Score 59; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels Ouery Match
Best Local Similarity 100...
Best Acad 9; Conservative RCICSHLWM 937 1 RCICSHIWM 9 929 8 셤

RESULT 15 ADR0083

ADR00838 standard; peptide; 9 AA. (first entry) ADR00838;

04-NOV-2004

Human 254P1D6B peptide SEQ ID NO:249.

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; chromosome 6.

Homo sapiens.

WO2004067716-A2

12-AUG-2004.

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P

(AGEN-) AGENSYS INC.

Ge ₩; Jakobovits A, Challita-Eid PM, Perez-Villar JJ, Faris M; Kanner SB, Raitano AB,

WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Example 9; SEQ ID NO 249; 345pp; English.

ö The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PlD6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous mucleotides in length. Also described: (I) a composition that comprises, consists essentially of, or consists es a peptide of eight, nine, ten, on eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID

any of the 42 lists of peptides, given in the specification, or a protein any of the 42 lists of peptides, given in the specification, or a protein that is at least 89, 91, 92, 93, 94, 95, 96, 97, 98, on 99* homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide that as a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5) generating a mammalian immune response directed to the protein of 8 confecting, in a sample, the presence of a 254PlD6B-related polynucleotide; (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human composition that composition and P1; (7) a pharmaceutical confidence that produces the antibody; (11) delivering a cytotoxic agent on non-human transgenic animal that produces the antibody; (10) a photosic of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1; 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful contracting and detecting cancer. The present sequence represents the human 254PlD6B peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22. %\$GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

Sequence 9 AA;

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ö 0; Indels Length 9; 1.1%; Score 59; DB 8; Le 100.0%; Pred. No. 1.8e+06; tive 0; Mismatches 0;

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254PlD6B-related polynucleotide, (6) a composition that modulates the status of a cell that expresses a protein of Pl; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (10) a diagnostic agent to a cell that expresses the protein of Pl; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of Pl. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B v.5, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22. 8888888888888888888888888

Sequence 1072 AA;

ô Gaps ö Score 5576; DB 8; Length 1072; Pred. No. 0; Mismatches 3; Indels 0; 99.98; Best Local Similarity 99.7 Matches 1069; Conservative Query Match

9 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTPPVVDCTAA Н

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9 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTPPVVDCTAA CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 61

CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLIFVIRPVQRPAQLLDYGDMM LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA 61 121

240 EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT 121

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300 EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPEPT TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST 181 241

EHSI PTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNII ITLPDNEVELKAFVAP TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP 301 301

APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLANLSQLSVGLYVFKVTVSSENAFGEGFV 361 361

540 KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALI VNNAVDYPPVANAGPNHTIT 481 481

LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTPQLK LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK VTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW 541 541 601

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VIDSSRQQSTAVVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR HVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN 601 661 661 721

1020 960 900 960 LIPKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT 961 VLAFTLIVLTGGFTWLCICCCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 961 VLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNWDEQERMELRPKYGIKHRST LAVILINVI.DSDI KVOKIRAHSDI.STVI VFYVOSRPPFKVI.KAABVARNI.HMRI.SKEKADF LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT 1021 EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1021 841 901 901 셤 쉽 셤 Š 성 암 g ò ઠ

ADR00601 standard; protein; 1072

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ADR00601;

04-NOV-2004 (first entry)

Human 254P1D6B v.6 protein SEQ ID NO:12.

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.6; chromosome 6.

Homo sapiens.

WO2004067716-A2

12-AUG-2004.

300 360 360 420

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P

(AGEN-) AGENSYS INC.

420

3 g Challita-Eid PM, Kanner SB, Raitano AB, Jakobovits A, Perez-Villar JJ, Faris M;

WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting protein or corresponand treating cancer.

Example 1; SEQ ID NO 12; 345pp; English.

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID NO:3, 5 or 7 ABNO0592, ABRO0594 or ABRO0596), or a peptide infolded in any of the 42 lists of peptides, given the specification, or a protein chat is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5)

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detecting, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related polynuclectide; (6) a composition that modulates the catatus of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cyctotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B v.6, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
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Sequence 1072 AA,

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ö 180 120 120 240 240 300 300 360 360 420 420 480 480 540 540 900 LPQNSITLNGNGSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK 600 999 99 EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR 720 ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN 780 9 9 KTSVDSPVLRLESNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM LINRGSPSGIWGDSPEDIRKDLPFLGKDWGLEEMSEYADDYRELEKDL1QPSGKQEPRGSA EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV VTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW EHVRGPSAVEMENI DKA LATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALI VNNAVDYPPVANAGPNHT1T LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK Gaps ; 0 Length 1072; Indels 3; . 8 DB Query Match
99.9%; Score 5574; E
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 541 Н 61 61 121 121 181 181 241 241 301 361 361 421 481 481 541 601 601 661 661 721 301 g

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VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020
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                                     LVEGVYTFHLRVIDSQGASDIDTATVEVQPDPRKSGLVELILQVGVGQLIEQRKDTLVRQ
                                                                                                                                                                     LAVLLINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF
                                                                                                                                                                                                                                                              LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT
                                                                                                                                                                                                                                                                                               961 VLAFTLIVLTGGFTWLCICCCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST
LVEGVYTFHLRVTDSQGASDTDTATVBVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ
                                                                                                                                LAVLLINVLDSD1KVQK1RAHSDLSTV1VFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF
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254PID6B-related protein; cytostatic; gene therapy; cancer; human;
254PID6B v.1 clone LCP-3; chromosome 6.
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Perez-Villar JJ, Faris
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generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PloB-related protein or a 254PloB-related polyucleotide; (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cyctoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and cl. 2) inhibiting growth, reproduction or survival of cancer cells that expresses the protein of P1. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful cor treating and detecting cancer. The present sequence represents the human 254PlD6B v.1 clone LCP-3, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome
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                                                                                                   LAVILINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF
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ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN
                                                                                                                                                                                  LAVILINVI.DSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVI.KAAEVARNI.HMRLSKEKADF
                                                                                                                                                                                                                                                                                                                LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCI CSHLWMENLIQRYIWDGESNCEWSI FYVT
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254PID6B-related protein; cytostatic; gene therapy; cancer; human;
254PID6B v.2; chromosome 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 254PlD6B v.2 protein SEQ ID NO:9
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Perez-Villar JJ, Faris
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that encodes the protein; (3) a composition comprising a polymucleotide that is a full complement of the polymucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5) generating, in a sample, the presence of a 254P106B-related protein or a 254P106B-related protein or a 254P106B-related protein or a camposition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254P106B has cytostatic activity, and can be useful for treating and detecting cancer. The present sequence represents the human 254P106B v.2, which is used in the exemplification of the present invention. The human 254P106B gene is located on chromosome 6p22.

Sequence 1072 AA;

ö Gaps ö 8; Length 1072; Indels ë, Score 5574; DB Pred. No. 0; 0; Mismatches Query Match 99.9%; Best Local Similarity 99.7%; Matches 1069; Conservative (

1 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA

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9 1 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA

180 LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA 121

180 121 LNRGSPSGIWGDSPEDIRKDLPFLGKDWGLEEMSEYADDYRELEKDLLQPSGKQEPRGSA

EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP 360 EHSI PTPPTSAAPSESTPSELPI SPTTAPRTVKEL TVSAGDNLI ITLPDNEVELKAFVAP 301 301

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APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV 420 361 APPUETTYNYEWNLISHPIDYQGEIKQGHKQTIANLSQLSVGLYVFKVTVSSENAFGEGFV 361

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540 540 9 KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALI VNNAVDYPPVANAGPNHTIT KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK 481 541 481

LPONSITLNGNOSSDDHQIVLYEWSLGPGSEGKHVVWQGVQTPYLHLSAMQEGDYTFQLK

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EHVRGPSAVEMENI DKA I ATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR

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VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020 LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT 960 780 900 900 LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT LAVLLINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF 961 VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTLLDNMDEQERWELRPKYGIKHRST LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ LAVILINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 841 . 196 721 781 841 901 901 1021 1021 781 용 g 유 g à 임 ઠે ò ð ò

RESULT 6 ADR00848

ADR00848 standard; protein; 1072 AA

ADR00848;

(first entry) 04-NOV-2004 Human 254PlD6B v.1 amino acid sequence SEQ ID NO:259.

254PiD6B; small interfering RNA; siRNA; immune response; 254PiD6B-related protein; cytostatic; gene therapy; cancer; human; 254PiD6B v.1; chromosome 6.

Homo sapiens.

WO2004067716-A2

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L2-AUG-2004.

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P.

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(AGEN-) AGENSYS INC.

3 æ Challita-Eid PM, Jakobovits A, M; Kanner SB, Raitano AB, Perez-Villar JJ, Faris

WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Example 13; SEQ ID NO 259; 345pp; English.

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to 254PID6B protein, oper reading frame (ORF) sequence which encodes the 254PID6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID NO:3, sor 7 ANROGS22, ANROGS24, or ABROGS26), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or

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identical to an entire amino acid sequence of Pi; (2) a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide described above; (4) generating a mammalian immune response directed to the protein of Pi; (5) detecting, in a sample, the presence of a 254P106B-related protein or 254P106B-related polynucleotide; (6) a composition that modulates the 254B106B-related polynucleotide; (6) a composition that modulates the 254B106B-related polynucleotide; (6) a composition that modulates the 254B106B and antibody or its fragment, which is monoclonal; (9) anno-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pi; and can be express the protein of Pi. 254P106B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a cempalification of the present invention. The human 254P106B gene is coated on chromosome 6p22.
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180 360 360 420 480 540 009 900 9 720 420 540 240 240 300 300 480 99 TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALI VNNAVDYPPVANAGPNHTIT LPONSITLINGNOSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT BYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELIVSAGDNLIITLPDNEVELKAFVAP APPVETTYNYEWNL1SHPTDYQGE1KQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV 361 APPVETTYNYEWNLISHPIDYQGEIKQGHKQTLANLSQLSVGLYVFKVTVSSENAFGEGFV NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE NYTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK VTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW VIDSSRQOSTAVVIVIVOPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR 181 241 541 181 301 661 121 241 421 481 541 601 601 301 361 421 481

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The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to 254PID6B cated open reading frame (ORF) sequence which encodes the 254PID6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous mucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID 780 840 840 900 900 960 960 New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer. LIFRVIRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN LVEGVYTPHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ LAVLLINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 961 VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN LAVILINVI, DSD I KVOKI RAHSD LSTVI VFYVOSR PPFKVI, KAAEVARNI, HMRLISKEKAD F 254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.2; chromosome 6. EHNSSLAVSESEFDSDQDTIFSREKAERGNPKVSMAGSIRNGASFSYCSKDR 1072 3 EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR g Challita-Eid PM, Human 254P1D6B v.2 protein SEQ ID NO:5. Jakobovits A, M; Claim 1; SEQ ID NO 5; 345pp; English. Ŕ ADR00594 standard; protein; 1072 23-JAN-2004; 2004WO-US001965 24-JAN-2003; 2003US-0442526P 04-NOV-2004 (first entry) Perez-Villar JJ, Faris Raitano AB, (AGEN-) AGENSYS INC. WPI; 2004-580991/56. N-PSDB; ADR00593 WO2004067716-A2 sapiens 12-AUG-2004. Kanner SB, 841] 1021 ADR00594; 901 961 841 1021 721 781 901 721 Homo RESULT 7 원 g 셤 임 ઠે δ g ð ò 셤 ò

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Sequence 1072 AA;

Gaps °; Length 1072; Indels 3; .. B 0; Mismatches Score 5574; Pred. No. 0; 99.94; Query Match Best Local Similarity 99.7 Matches 1069; Conservative

1 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA

RESULT

9 1 MAPPIGVLSSLLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA

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LPONSITLNGNOSSDDHQIVLYEMSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK 600 VTDSSRQQSTAXVTV1VQPENNRPPVAVAGPDKEL1FPVESATLDGSSSSDDHG1VFYHW 541 601

EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR 720

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VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020 720 780 780 840 900 900 960 ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN LVEGVYTFHLRVTDSQGASDTDTATVEVQPPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ LAVLLINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST LVEGVYTPHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 901 961 1021 1021 721 781 901 961 781 841 841 199 721 셤 g ઠે 셤 ઠે g ò 요 ò 셤 ò ઠે

254PlD6B; small interfering RNA; siRNA; immune response; 254PlD6B-related protein; cytostatic; gene therapy; cancer; human; 254PlD6B v.1 clone LCP-3; chromosome 6. Human 254PlD6B v.1 clone LCP-3 protein SEQ ID NO:3. ADR00592 standard; protein; 1072 AA (first entry) 04-NOV-2004 ADR00592;

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23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P. (AGEN-) AGENSYS INC

3 ge Challita-Eid PM, Jakobovits A, M; Kanner SB, Raitano AB, Perez-Villar JJ, Faris WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B N-PSDB; ADR00591

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or corresponds to a subsequence of the ORF, useful for detecting
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Claim 1; SEQ ID NO 3; 345pp; English.

The present invention describes a 254P1D6B small interfering RNA (SIRNA) Composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the control of coid open reading frame (ORF) sequence which encodes the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous contiguous anno acids of a protein of figure 2 (Pl, see SEQ ID nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or consists essentially of, or consists of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADRO0552, ADRO0559, or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) conference of a 254P1D6B-related protein or a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that expresses the protein of P1; and con-human transgenic animal that expresses the protein of P1; and con-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and con-human transgenic animal that produces the antibody; (11) delivering a cytostatic activity, and can be composition or survival of cancer cells that express the protein of P1; 254P1D6B has cytostatic activity, and can be composition and methods are useful for treating and detecting cancer. The present sequence represents the human 254P1D6B v1 clone LCP-3, which is used in the exemplification of creating an expression of control of control of control of c

Sequence 1072 AA;

ö Gaps ö DB 8; Length 1072; 0; Indels 99.9%; Score 5574; D 100.0%; Pred. No. 0; ive 0; Mismatches Best Local Similarity 100. Matches 1072; Conservative Query Match

240 420 240 300 300 360 360 420 480 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 120 LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA 180 9 EHSI PTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLI TLPDNEVELKAFVAP CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEBINGPFIEE 1 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTPPVVDCTAA **EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT** TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST 241 TPSSGEVLEKEKASOLOEOSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE 61 181 301 121 241 61 181 301 361 421 a 셤 q а 셤 ò ద ò g ò ò ઠે à ò

961 VLAFTLIVLTGGFTWLCICCCCKROKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020 961 VLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020 99 540 900 99 720 780 780 840 840 900 900 960 901 LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT 960 841 LAVLLINVIDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGRHVVMQGVQTPYLHLSAMQEGDYTFQLK EHVRGPSAVEMENI DKAI ATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN 721 ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ 781 LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGVGQLTEQRKDTLVRQ LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK VTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELI PPVESATLDGSSSSDDHGIVFYHW EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR LAVLLINVLDSD1KVQK1RAHSDLSTV1VFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF EHNSSLMVSESEFDSDODTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 EHNSSLAVSESEPDSDQDTIFSREKAERGNPKVSMAGSIRNGASFSYCSKDR 1072 Human 254P1D6B v.1 protein sequence SEQ ID NO:273. ADR00862 standard; protein; 1053 AA. 04-NOV-2004 (first entry) ADR00862; 1021 781 1021 541 541 601 601 661 661 721 841 901 481 RESULT g g 셤 g g 셤 a ઠે ద ò 셤 8 요 8 8 ઠે ઠ ઠે ð

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.1; chromosome 6. Homo sapiens.

Challita-Eid Kanner SB, Raitano AB, Jakobovits A, Perez-Villar JJ, Faris M; 23-JAN-2004; 2004WO-US001965 24-JAN-2003; 2003US-0442526P (AGEN-) AGENSYS INC.

WO2004067716-A2

12-AUG-2004.

WPI; 2004-580991/56.

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New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                     and treating cancer.
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Example 5; SEQ ID NO 273; 345pp; English.

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the consists acid open reading frame (ORF) sequence of the concision that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 [Pl. see SEQ ID NO:3, 5 or 7 AbR00592, AbR00594 or AbR00566), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of Pl; (2) a polynucleotide that is a feat be protein; (3) a composition comprising a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of Pl; (5) generating in a sample, the presence of a 254PID6B-related protein or a 254PID6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition described above; (10) a non-human transgenic animal that expresses a protein of Pl; (7) a pharmaceutical composition at a diagnostic agent to a cell that expresses the protein of Pl; (10) a non-human transgenic animal that expresses the protein of Pl; (10) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pl; and composition or survival of cancer cells that expresses the protein of Pl; and composition or survival of cancer cells that express the protein of Pl; 254PID6B has cytostatic activity, and can be human 254PID6B vertices which is used in the exemplification or confidence or processes the protein sequence, which is used in the expressible or protein sequence, which is used in the expressibility of the present invention. The human 254PID6B gene is located to be protein or protein sequence.

Sequence 1053 AA;

Gaps ô 8; Length 1053; Indels 3 Score 5485; DB Pred. No. 0; 0; Mismatches 98.3%; Best Local Similarity 99.7 Matches 1050; Conservative Query Match

VSCPHKENCEPKKWGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK 139 79 9 CARKOCSEGRIYSNAVISPNLETIRIMRVSHTFPVVDCTAACCDLSSCDLAWFEGRCYL CARKOCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL 20 80 셤 8 ઠે

DLPFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV

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GDSPAVPAETQODPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS GDSPAVPABTQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEXEKASQLQEQ 200 181 260

240 319

180 259

SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS ELPI SPTTAPRIVKELIVSAGDNLI I TLPDNEVELKAFVAPAPPVETTYNYEMLISHPT ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT 241 301 320

440 PQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNY 499 DY OGEIK OGHKOTLALSQLSVGLYVFKVTVSSENA FGEGFVNVTVKPARRVALPPVAVVS 361

DYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVS

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CCKRQKRIKIRKKTKYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDT 1020 CCKROKRIKIRKKIKYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDT 1039 919 900 979 901 HGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCIC 960 480 540 619 9 619 9 739 720 799 780 DIDIAIVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA 859 840 HSDLSTVIVFYVQSRPPFKVLXAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSG TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS DIDIATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPINNSITLD HGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCIC VLYEWSLGPGSEGKHVVWQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAVVTVVV ENNRPPVAVAGPDKEL1FPVESATLDGSSSSDDHG1VFYHWEHVRGPSAVEMEN1DKA1A GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS HSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSG SFRLIVIDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQP IFSREXMERGNPKVSMNGSIRNGASFSYCSKDR 1072 1040 860 841 980 961 481 260 541 620 680 740 800 781 920 200 601 661 721 421 ò 셤 ò 셤 ò 셤 ઠે q ò 셤 ઠ g ò 셤 ò 원 ઠ g ò

Z ADR00863 standard; protein; 1053 04-NOV-2004 (first entry) ADR00863; RESULT 10 ADR00863

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254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.3; chromosome 6. Homo sapiens.

Human 254P1D6B v.3 protein sequence SEQ ID NO:274.

WO2004067716-A2 12-AUG-2004.

24-JAN-2003; 2003US-0442526P. (AGEN-) AGENSYS INC.

23-JAN-2004; 2004WO-US001965.

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3 e Challita-Eid PM, Jakobovits A, Kanner SB, Raitano AB, Ja Perez-Villar JJ, Faris M;

2004-580991/56

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the capture acid open reading frame (ORF) sequence which encodes the capture the nuclectides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID CO CONSISTS ADRO0594). ADRO0595, or a peptide in included in any of the 42 lists of peptides of a protein of figure 2 (Pl, see SEQ ID CONSISTS OF 7 ADRO0595), or a peptide included in any of the 42 lists of peptides given in the specification, or a protein cany of the 42 lists of peptides of sequence of Pl; (2) a polynucleotide that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or confined to an entire amino acid sequence of Pl; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) detecting a mammalian immune response directed to the protein or a 244D106B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition that comprises the composition that comprises the composition does form; (8) an antibody or its fragment, which is monoclonal; (9) which does form; (8) an antibody or its fragment, which is monoclonal; (9) which does form; (9) an antibody or its fragment, which is monoclonal; (10) a pharmaceutic or a conformation animal that produces the antibody; (10) a pharmaceutic or a composition that modulates the composition animal that produces the antibody; (10) a pharmaceutic or a composition that composition animal that produces the antibody; (10) a pharmaceutic or a composition animal that produces the antibody; (10) a pharmaceutic or a composition animal that produces the antibody; (10) a pharmaceutic or a composition animal that produces the anon-than animal that produces the animal animal that produces the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hybridoma that produces the antibody; (11) delivering a grotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254P106B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254P106B v.3 protein sequence, which is used in the exemplification of the present invention. The human 254P1D6B gene is located on
                                                                      New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                              Example 5; SEQ ID NO 274; 345pp; English.
                                                                                                                                                                                        treating cancer.
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8 Score 5485; DE Pred. No. 0; 0; Mismatches 98.3%; Conservative Similarity Sequence 1053 AA Matches 1050; Query Match Local

ö 80 VSCPHKENCEPKKWGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK 139 180 259 240 SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS 319 SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS 300 379 360 DYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVS 439 DLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV 199 1 CARRQCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL 60 GDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ ELPISPTTAPRTVKELTVSAGDNIIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT CARKQCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL DLPFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV GDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ **ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT** Gaps ö 8; Length 1053; Indels 3, 61 320 20 260 241 301 380 140 121 200 181 셤 ద 8 셤 δ 8 8 6 8 상 원 ਨੇ

1039 1020 840 900 979 499 480 559 540 619 900 619 739 720 799 780 859 919 960 VLYEWSLGPGSEGKHVVWQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQSTAVVTVIVQP DIDIAIVEVQPDPRKSGLVELILQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA CCKROKRIKIRKKTKYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDT 601 ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLINLVEGVYTFHLRVTDSQGAS HSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSG HGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCIC HGHCDPLTKRCICSHLMMENLIQRYIMDGESNCEWSIFYYTVLAFTLIVLTGGFTWLCIC PQLQELTLPLTSALIDGSQSTDDTEIVSYHWEBINGPFIEEKTSVDSPVLRLSNLDPGNY SFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI SFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPONSITLNGNOSSDDHOI VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQP ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA TVTGL,QVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS DIDIATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA POLOELTLPLTSALIDGSOSTDDTEIVSYHWEEINGPFIEBKTSVDSPVLRLSNLDPGNY 254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.3; chromosome 6. Human 254P1D6B v.3 protein sequence SEQ ID NO:272. 1040 IFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 1021 IFSREXMERGNPKVSMNGSIRNGASFSYCSKDR 1053 ADR00861 standard; protein; 1063 AA (first entry) 04-NOV-2004 440 421 200 481 260 541 620 680 740 721 800 781 860 841 920 901 980 셤 셤 셤 ठे g 8 셤 8 셤 8 셤 ઠે 원 8 8 원 ઠે 셤 8 셤 ઠે 8

24-JAN-2003; 2003US-0442526P. 23-JAN-2004; 2004WO-US001965 (AGEN-) AGENSYS INC. WO2004067716-A2 Homo sapiens 12-AUG-2004 ADROUGE 11
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Ge ₩;

Challita-Eid PM,

Jakobovits A,

Raitano AB,

SB,

Kanner

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The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the controlled siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous controlled siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous contiguous animo acids of a peptide of eight, nine, ten, or consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADRO0592, ADRO0594 or ADRO0556), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein chat is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of Pl; (2) a polymucleotide that is a full complement of the polymucleotide described above; (4) confined in a sample, the presence of a 254PID6B-related protein or a cell that expresses a protein of Pl; (7) a pharmaceutical composition that modulates the composition that comprises the composition that modulates the composition that comprises the composition of Pl; (7) a pharmaceutical composition that comprises the protein of Pl; (7) a pharmaceutical composition that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pl; and con the protein of Pl; and or a diagnostic agent to a cell that expresses the protein of Pl; and con-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pl; and corressents a must be a protein of Pl; and protein of Pl; and present ingent therapy. The composition or survival of cancer cells that expressent sequence represent sequence represent invention. The human 254PID6B gene is located on
                                                                                                          New 254FID6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254FID6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                                                                                                                                                                     Example 5; SEQ ID NO 272; 345pp; English.
Faris
                                                      2004-580991/56.
Perez-Villar JJ,
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Sequence 1063 AA;

ö 71 VSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMALNRGSPSGIWGDSPEDIRK 130 199 259 319 SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS 310 379 370 380 DYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVS 439 VSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK 139 70 **ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT** ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT GDSPAVPAETQODPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS 20 CARKQCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL DLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV Gaps ö 8; Length 1063; ., E 98.3%; Score 5485; DB 99.7%; Pred. No. 0; 0; Mismatches Best Local Similarity Matches 1050; Conservative Similarity 80 311 200 260 251 320 140 191 Query Match 셤 임 셤 셤 ò 8 Š ઠે ద ò δ

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VLYEWSLGPGSEGKHVVWQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAVVTVVVV
                                                                                                                                                                                      ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA
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                                                                                                                              VLYEWSLGPGSEGRHVVMOGVOTPYLHLSAMOEGDYTFOLKVTDSSROOSTAXVTVIVOP
                                                                                                                                                                         ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA
                                                                                                                                                                                                                      TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD
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                                    PQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNY
                                                                               SFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI
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254PID6B; small interfering RNA; siRNA; immune response; 254PID6B-related protein; cytostatic; gene therapy; cancer; human; 254PID6B v.3; chromosome 6. Human 254P1D6B v.3 protein SEQ ID NO:7. ADR00596 standard; protein; 1063 AA 23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P. (first entry) WO2004067716-A2 Homo sapiens 04-NOV-2004 12-AUG-2004. 셤

(AGEN-) AGENSYS INC.

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254P1D6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists as length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pt, see SEQ ID NO:3, 5 or 7 ADRO0592, ADRO0594 or ADRO0596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein cot that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98* homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) cannow that is a full complement of the polynucleotide described above; (4) cannow that is a sample, the presence of a 254P1D6B-related protein or a 254P1D6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition described above; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (11) delivering a cytocoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and con-human transgenic animal that produces the antibody; (11) delivering a cytocoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and con-human integration or survival of cancer cells that expresses the protein of P1. 254P1D6B has cytostatic activity, and can be cased in gene therapy. The composition or survival of cancer cells the human 254P1D6B with the exemplification of the present concepted to the present of the present in the exemplification of the present concepted in the exemplification of the present concepted in the exemplification. The human 254P1D6B gene is locate
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                                                                                                                                            New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
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                      Challita-Bid PM,
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99.7%; Pred. No. 0;
ive 0; Mismatches
                      Jakobovits A,
                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 7; 345pp; English.
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Best Local Similarity 99.7
Matches 1050; Conservative
                    Kanner SB, Raitano AB,
Perez-Villar JJ, Faris
                                                                                                                                                                                      protein or corresponand treating cancer.
                                                                                WPI; 2004-580991/56.
N-PSDB; ADR00595.
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                                                                                                                                                                                                                    611 ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA
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DYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVS
                                                PQLQELTLPLTSALIDGSQSTDDTEIVSYHWEBINGPFIEBKTSVDSPVLRLSNLDPGNY
                                                                                                                                                   VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQP
                                                                                                                                                                                                      ENNR PPVAVAGPDKELI FPVESATLDGSSSSDDHGI VFYHWEHVRGPSAVEMENI DKAIA
                                                                                                                                                                                                                                                        TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD
                                                                                                                                                                                                                                                                                                          GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS
                                                                                                 500 SFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254PID6B; small interfering RNA; siRNA; immune response;
254PID6B-related protein; cytostatic; gene therapy; cancer; human;
254PID6B v.3; chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1040 IFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072
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311 ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT

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New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                 Challita-Eid
                 Jakobovits A,
                       Faris M;
                 Raitano AB,
                                  2004-580991/56.
      (AGEN-) AGENSYS INC
                       Perez-Villar JJ,
                 Kanner
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Example 1; SEQ ID NO 10; 345pp; English.

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the corresponds to a subsequence of the ORF, where the acid open reading frame (ORF) sequence which encodes the complete stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists assentially of or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO.3, 5 or 7 ADRO0592, ADRO0594 or ADRO0596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein contact is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 934 homologous or identical to an entire amino acid sequence of Pl; (2) a polymucleotide that is a full complement of the polymucleotide described above; (4) composition in a sample, the presence of a 254PID6B-related polymucleotide; (6) a composition that modulates the composition that comprises the composition that modulates the composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a phyrident of the protein of the pro or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B v.3, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.

Sequence 1063 AA;

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                                                              CARKQCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL
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Score 5485; DB 8; Length 1063; Pred. No. 0; 0; Mismatches 3; Indels 0;
98.3%;
                                 Matches 1050; Conservative
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CCKROKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDT 1039 antidiabetic; cytostatic; dermatological; immunosuppressive; antidiabetic; cytostatic; dermatological; immunosuppressive; antidiabetic; cytostatic; dermatological; immunosuppressive; antidiamatory; thyromimetic; antiallergic; cerebroprotective; antiparkinsonian; antibacterial; antiparsitic; anticonvulsant; antiparkinsonian; antibacterial; antiparsitic; fungicide; protozoacide; virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV; notoropic; neurodegenerative; Parkinson's disease; Alzheimer's; muscular; myotonic dystrophy; catatonia; endocrine; diabetes; Grave's; leukaemia; cervical; breast cancer; immunological; scleroderma; cystemic lupus erythematosus; allegy; gastrointestinal; Crohn's; renal; Goodpasture's syndrome; viral infection; bacterial; fungal; parssitic; protozoal; helminthic; cardiovascular; atherosclerosis; hepatic; 490 979 430 499 559 550 619 610 619 670 739 730 799 790 859 850 919 910 911 HGHCDPLTKRCICSHLAMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCIC 970 ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA DTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA SFRLIVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQP VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAVVTVIVQP ENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIA TVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLD HGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCIC DYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVS POLOELTLPLTSALIDGSOSTDDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNY SFRLTVTDSDGATNSTTAALI VNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI GSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGAS DIDIATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRA HSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSG 1040 IFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 ADG14994 standard; protein; 978 (first entry) Human SECP-27 protein. 26-FEB-2004 440 1031 ADG14994; 491 260 791 860 851 200 551 620 680 740 800 920 980 971 380 611 671 731 RESULT 14 ADG14994 g g 셤 à 셤 Š g Š 셤 ð 셤 ઠ 셤 a qq 셤 ò ò 셤 ò δ ઠ ò Š

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                                                                                                                                                                                        LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ
                                                                                                                                                                                                                                                                     361 APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV
                                                                                                                                                                                                                                                                                                                          NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE
                                                                                                                                                                                                                                                                                                                                                   KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAVILINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF
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                                                                                                                 TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST
                                                                                                                                                                      EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP
                                                                                                                                                                                                                                                 361 APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV
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                EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine SST20-6 protein related to adipocyte function SeqID 22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel isolated SECP (secreted protein)

Complypeptide. The polypeptide of the invention demonstrates

Comeroprofective, relaxant, antithyrodd, antidiabetic, cytostatic,

dermatological, immunosuppressive, antiinflammatory, thyromimetic,

antiallergic, cerebroprotective, gastrointestinal, hepatotropic,

compliant anticonouslant, antiparkinsonian, antibacterial,

antiparasitic, fungicide, protozoadide, virucide, uropathic,

antirheumatic, cardiant, cardiovascular, anti-HIV and nootropic,

antirheumatic, cardiant, cardiovascular, anti-HIV and nootropic

continities. The polypeptide may be useful in diagnoshing, preventing and

treating disorders including neurodegenerative disorders such as

Compotonic dystrophy and catatonia, endocrine disorders particularly

chotosomy and Grave's disease, cancers such as leukaemia, cervical or

breast cancer, immunological disorders including scleroderma, systemic

chreates and Grave's disease, cancers such as leukaemia, cervical

chous srythemacrosus and allergies, gastrointestinal disorders

continually Crohn's disease, renal disorders eg. Goodpasture's

cyndrome, infections particularly viral, bacterial, fungal, parasitic,

protozoal, helminthic, cardiovascular disorders including atherosclerosis

and hepatic diseases particularly cirrhosis. The polynucleotides may be

cused to create humanised or transgenic animals, as well during gene

cused to create humanised or transgenic animals, as well during gene

charactical and animal and animals and animals and animals and animals and animals and animals and animals and animals and animals animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer
                                                                                                                                                                                                                                                                                                                              Marquis JP, Lee SY, Elliott VS, Ramkumar J, Hafalia AJA;
Kable AB, Chawla NK, Emerling BM, Khare R, Jiang X, Jackson AA;
Hawkins PR, Jin P, Mason PM, Richardson TW, Swarnakar A, Lal PG;
Warren BA, Lee S, Griffin JA, Fu GK, Wilson AD, Xu Y, Bulloch S,
Becha SD, Bhatia UG, Burrill JD, Blake JJ, Ho A, Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 4938; DE; Pred. No. 0; 1; Mismatches
gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 27; 300pp; English.
                                                                                                                                                                                        05-APR-2002; 2002US-0370707P.
19-APR-2002; 2002US-0373824P.
03-MAY-2002; 2002US-0377883P.
24-MAY-2002; 2002US-0383218P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.5%;
                                                                                                                                                      2003WO-US010249
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  cirrhosis; transgenic;
                                                                                                                                                                                                                                                                                            (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-845310/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. neuromuscular and/or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADG15055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 978 AA;
                                                                           WO2003087300-A2.
                                                                                                                                                    01-APR-2003;
                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 949;
                                                                                                               23-OCT-2003
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Matches
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This invention relates to novel membrane proteins that are associated with differentiation and/ or metabolic function of adipocytes, in particular of mouse origin. Specifically, it refers to the isolated nucleic acid molecules encoding all or part of these proteins, appropriate antibodies and screening assays useful for the development of drug compositions derived thereof. The present invention describes these compositions as useful for the treatment of diseases associated with abnormalities of adipocyte function, such that they can be used to prevent, treat or diagnose obesity, hypertension, hyperlipaemia, diabetes and arteriosclerosis. Accordingly, they exhibit anorectic, antidiabetic, antiarteriosclerotic, antilipaemic and hypotensive activities. This polypeptide is a murine membrane protein sequence related to adipocyte function of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVLWLSTDADESR--COOGKTLYGAGLRTEGE-NHLRLLAGSLPFHACRAACCRDSACHA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 GSAEYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELH-----YLNESASTPAPKLP
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43.5%; Score 2426.5; DB 8; Length 1048;
Best Local Similarity 48.1%; Pred. No. 4.4e-168;
Matches 519; Conservative 136; Mismatches 314; Indels 109; Gaps
                                                                                                                                                                                                                                                      Mouse membrane and secretory proteins of adipocyte origin and polynucleotides encoding them for screening compounds as remedies for obesity, diabetes, arteriosclerosis, hypertension and hyperlipemia.
                                                                                                                                                Furuyama N;
                                                                                                                                                Matsuzawa Y, Funahashi T, Shimomura C,
                                                                                                                                                                                                                                                                                                                                          Claim 41; SEQ ID NO 22; 195pp; Japanese
                      09-JUL-2003; 2003WO-JP008690
                                                              10-JUL-2002; 2002JP-00201856
                                                                                                      (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                        WPI; 2004-122943/12.
N-PSDB; ADM36226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1048 AA;
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DGESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMDEQER 1006 739 826 859 919 977 586 646 619 706 619 994 799 827 GQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVA 886 887 RNIHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIW 946 1007 MELRP--KYCIKHRSTEHNSSLMVSESEFDSDODTIFSREKMERGNPKVSMNGSIRNG 1062 AMIKSELQKQKADFLIFRALEISTVTCQLNCSDHGHCDSFTKRCVCDFFWMENFIKVQLR LSAMQEGDYTFQLKVIDSSRQSTAXVIVUQPENNRPPVAVAGPDKELIFPVESATLDG SSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTST IDGSDHSVALQLTNLVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGV YPPVANAGPNHTITLPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLH LTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDV 260 680 740 920 620 947 978 587 647 167 527 707 g ð a ð g g ò 임 ò g ò 셤 8 g ò ઠે ò

Search completed: October 12, 2005, 10:02:48 Job time : 131 secs

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QYHWEELKGPLREEKISEDTAILKLSKLVPGNYTFSLTVVDSDGATNSTTASLTVNKAVD 499

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SYHWEEINGPPIEEKTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVD

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October 12, 2005, 10:00:24 ; Search time 128 Seconds (without alignments) 4288.663 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
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1 MAPPIGVLSSLLLLVTIAGC......VSMNGSIRNGASFSYCSKDR 1072 US-10-764-390-3 5580 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 Total number of hits satisfying chosen parameters:

1612378 seqs, 512079187 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0994g7 homo sapien 080u39 mus musculu 0718r6 homo sapien 08bhu7 mus musculu 08bhu7 mus musculu 08bhu7 mus musculu 08bhu7 homo sapien 08uy25 homo sapien 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 mus musculu 09hr9 musculu 09hr9 musculu 09hr9 musculu 09hr9 musculu 09hr9 musculu 09hr9 musculu 09hr9 homo sapien 09frza drosophila 09filo homo sapien 09f Description 091467 080139 080136 081136 081137 081127 081127 081128 081128 081128 081128 081128 081128 081128 081128 081128 081128 081128 081128 081128 081128 Query Match Length DB Score Resunt.

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2 Q6VBJ3	2 Q7WN54	2 Q7PC51	2 Q693B8	2 Q9AER7	2 Q6VBI8	2 Q7KQP5	2 Q7KQP6	2 Q7KQP7	2 Q9V4F7	2 Q6VBJ4	2 Q74BT1	2 Q74BG8	2 Q8ZKG6
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ALIGNMENTS

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TPSSGEVLEKEKAAQLQEQSSNSSGKEVLAPSHSLPPASLELSSVTVEKSPVLTVTPGST
                                                                                                                                  APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV
                                                                                                                                                            APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSENAFGEGFV
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MKIAA0319 protein (Fragment).
Name=D130043K22Rik; Synonyms=mKIAA0319;
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Mus musculus (Mouse). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090,

SEQUENCE FROM N.A. TISSUE=Brain; MEDLINE=22579291; PubMed=12693553;

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350
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CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 120
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                                                                                                                                                                                                    Gaps
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                                                                                                                                                                              Score 4255.5; DB 2;
Pred. No. 2.5e-200;
1; Mismatches 160;
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75.8%;
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RD SEQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N. TISSUE=Kidney;

REAINE=FUB/N. TISSUE=Kidney;

REAINE=FUB/N. TISSUE=Kidney;

RA STRAINE=FUB/N. TISSUE=Kidney;

RA STRAINE=FUB/N. TISSUE-Kidney;

RA STRAINEFUB/N.C. Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetcow K. H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Rownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulky S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Witting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Mersywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Melecation and initial analysis of more than 15,000 full-length human
                241 RQQSTAVVIVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRG
                                                                              301 PSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGG
                                                                                                                                                                                                                                                                                                                                                                                                     421 YTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLL
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                                                             PSAVEMENIDIKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGG
                                                                                                                           RHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGV
                                                                                                                                            RHVLVLPNNSITLDGSRSTDDQRIVSYLMIRDGQSPAAGDVIDGSDHSVALQLTNLVEGV
                                                                                                                                                                                      786 YTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rođentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
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Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26, Expressed sequence AU040320.
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               EQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLH
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DHSVALQLTNLVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amotation update)
DJ73M23.3 (KIAA0319 gene product) (Fragment).
Home add73M23.3;
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Pred. No. 6.4e-172;
0; Mismatches 1;
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Best Local Similarity 99.9
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Heart;
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SEQUENCE FROM N.A.
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Name=AU040320;
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                                                                                                                                                                                                                   DB 2; Length 1048;
                                                                                                                                                                                                                / Match 43.5%; Score 2426.5; DB 2; Length Local Similarity 48.1%; Pred. No. 1.1e-110; Les 519; Conservative 136; Mismatches 314; Indels
                    to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                  F4D51DD6DE4C889D CRC64;
Strausberg R.;
Submitted (MAX-2002) to the EMBL/Ge EMBL, BC028869; AAH28869.1; -. MGD; MGI:2140475; AUG40320.
InterPro; IPR003961; FN III.
InterPro; IPR0008957; FN III-like.
InterPro; IPR000601; PNJ.
SMART; SM00669; FNJ; 4.
                                                                                                                                                                                  1048 AA; 115311 MW;
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SEQUENCE 1048 AA; 11
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920 DGDSNCEWSVLYVIIASFVIVVALGILSWTTICCCKRQK-GKPKRKSRXKILDATD-QES
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STRAIN=CSPEL/6J; TISSUB=Heart;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh N.
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10:1617-1630(2000).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriche
library, clone:D330027H07 product:HYPOTHETICAL 103.9 kDa PROTEIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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01-MAR-2003 (TrEMBLrel. 23, Created)
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01-MAR-2004 (TrEMBLrel. 26, Last ann
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STRAIN=CS7BL/6J; TISSUE=Cerebellum;
The FANTOM CONSORTIUM,
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
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SEQUENCE FROM N.A.
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                                                 C STRAIN=C57BL/GJ; TISSUB=Heart;
A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Hanagaki T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., A Hori F., Imotami K., Ishii Y., Itoh M., Kagawa T., Kadawa T., Kojima Y., Kondo S., Konno H., Kowda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Okaaki Y., A Nishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazaki Y., Salto R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Taya T., Yakanishi P., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 43.1%; Score 2403.5; DB 2; Length 1085; Best Local Similarity 48.3%; Pred. No. 1.6e-109; Matches 514; Conservative 135; Mismatches 307; Indels 109;
"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                SMART; SM00060; FN3; 4.
SMART; SM00089; FN3; 4.
SMART; SM00089; PKD; 5.
Hypothetical protein.
SEQUENCE 1085 AA; 119329 MW; 7E61DB6001A275E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 LWWLEGMCFQADCSKPQSCQPFRTDSSNSML-------
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                                                                                                                                                                                                                                                MGD; MGI:2140475; AU040320.
InterPro; IPR003954; FN III.
InterPro; IPR000957; FN III-like.
InterPro; IPR000601; PKD.
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                                                                                                                                              920 DGDSNCEWSVLYVIIASFVIVVALGILSWTTICCCKRQK-GKPKRKSRYKILDATD-QES
                                707 LTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDV
                                                                                                                                                                                                                                                         767 IDGSDHSVALQLINLVEGVYTFHLRVIDSQGASDTDIATVEVQPDPRKSGLVELTLQVGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     887 RNIJHMRISKEKADFLIFKVIRVDIAGCLIKCSGHGHCDPLIKRCICSHLWMENLIQRYIW
                                                                                                             SSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTST
LSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATLDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A730047D20 product:HYPOTHERICAL 103.9 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annotation of a full-length mouse cDNA collection.";
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STRAIN=C57BL/61; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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439 526 499 586 646

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DGESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQER 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOLTEORKOTLVROLAVLLNVLDSDIKVOKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVA 886
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                                                                                                                                           SYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVD
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                            LPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGE1KQGHKQTLNLSQLSVGLYVFK
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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LELKPTSRAGSKQKGPTLSSSLMHSESELDSD-DAIFTWPDREKG 1021
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amnotation update)
Polycystic kidney disease 1-like, isoform a.
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Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Murantsu N., Hayashizaki Y., Shibata K., Itoh M., Konno H., Okazaki Y., Murantsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/GJ; TISSUB=Cerebellum;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata Y., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumin N., Ishili Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamocto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Tozawa M., Ohara E., Watshikaya T., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 43.1%; Score 2403.5; DB 2; Length 1085; al Similarity 48.3%; Pred. No. 1.6e-109; 514; Conservative 135; Mismatches 307; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1085 AA; 119437 MW; 64CCADE9B26E84E0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                857 HEVAAMLKSELRKQKADFLIFRALEVNTVTCQLNCSDHGHCDSFTKRCICDFFWENFIK 916
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                               TLDGSKSSDDQKIISYLWEKTQGPDGVQLENANSSVATVTGLQVGTYVFTLTVKDERNLQ
                                                                                                                   SQSSVNVIVKEEINKPPIAKITGNVVITLPTSTAELDGSKSSDDKGIVSYLWTRDEGSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTL
                                                                                                                                                                                                       823 QVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKA
                                                                                                                                                                                                                                                                                          883 AEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             943 RYIWDGESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKROKRTKIRKKTKYTILDNMD
         TLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLS
                                                                                            STSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPA
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Polycystic kidney disease 1-related protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AXI63234; AAN61054.1; -.
InterPro; IPR00361; FN III.
InterPro; IPR000601; PKD.
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48.0%; Pred. No. 2e-109;
tive 134; Mismatches 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ĠFLPEDDVPHĽLGĽĠWNWA-----
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SMART; SM00089; PKD; 5.
PROSITE; PS50093; PKD;
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Best Local Similarity
Matches 519; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TEHSIPTP-----PTSAAPSESTPSELPISPTTAPRTVKELTVSAGDN 342
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan R.J., Malek J.B., Gunarerne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEFKVIVEGQNAHGEGYVNVTVKPEPRKNRPPIAIVSPQFQEISLPTTSTVIDGSQSTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHINGYHWEELKGPLREEKISEDTAILKLSKLVPGNYTFSLTVVDSDGATNSTTANLTVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLLLLVTIAGCARKQCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 GSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPER----SVLLPLPTTPSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------RPAVSSSDQQ-----SLIRKLQKRGSPSDVVTPIVTQHS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LI ITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.0%; Score 2402; DB 2; Length 10
Best Local Similarity 48.0%; Pred. No. 1.8e-109;
Matches 519; Conservative 134; Mismatches 313; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC014530; AAH14530.1; -...
InterPro; IPR006601; PKD.
SMART; SM00089; PKD; 5.
PROSITE; PS00039; PKD; 1.
SEQUENCE 1049 AA; 115584 MW; 5BDE6057CC09A649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (SEP-2001) to the
                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       TISSUE=Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                  162
                                                                                                                                                                                                                                                                                                                                                                                                                            -----TEHSIPTP-----PISAAPSESTPSELPISPTTAPRIVKELTVSAGDNL 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQR 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455 TLQLSAMQEGDYTYQLTVTDT1GQQATAQVTVIVQPENNKPPQADAGPDKELTLPVDSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 QITLPRNEVQLNAYVLQEPPKGETYTYDWQLITHPRDYSGEMEGKHSQILKLSKLTPGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESAT
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                                                                                                                                                                                                                                                                                                                     SECAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPER----SVLLPLPTTPSSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 IITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLY
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                                                                                                                                                                                                                                                                                Gaps
            Craniata, Vertebrata, Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                        95;
                                                (1)
SEQUENCE FROM N.A.
A GIN W.X., Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Zhao Qin W.X., Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Zhao Qin W.X., Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Zhao Wan D.F., Gu J.R.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR289597; AAL55781.1; -.
R SMART; SM00069; FN3; 4.
R SMART; SM00069; FN3; 4.
R PROSITE; PS50093; PKD; 1.
W HYPOCHAELICAL PACCES.
O SEQUENCE 946 AA; 103879 WW; B52C7F0BD0A60620 CRC64;
                                                                                                                                                                                                               2; Length
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                             41.5%; Score 2316.5; DB 2; ilarity 50.9%; Pred. No. 2.5e-105; Conservative 119; Mismatches 258;
         Chordata; (Primates; (
            Eukaryota; Metazoa;
Mammalia; Eutheria;
MCBI_TaxID=9606;
sapiens (Human)
                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 489;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQERMELRP -- KYGIKHRSTEHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIR 1060
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                                                                                                                                                           402
                                                                                                                                                                                                                                                                                            496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            823 QVGVGQLITEQRKDTLVRQLAVLLAVVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKA 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLMMENLIQ 942
                                                                                                                                                                                                               DINVSQLTERLKGMFIRQIGVLLGVLDSDIIVQKIQPYTEQSTKAVFFVQNEPPHQIFKG
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QQVKSSEKTQIAVPQPVAPSYSYATPTPQASFQSTSAPYPV-----IKELVVSAGES
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                         -----SLIRKLOKRGSPSDVVTPIVTQHS--
                                                    EVLEKEKASQLQEQSSNSSCKEVLMPSHSLPPASLELS-----SVTVEKSPVLTVTPGS
                                                                    -----PTSAAPSESTPSELPISPTTAPRTVKELTVSAGDN
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                          ------RPAVSSSDQQ-
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Q8WYZ5;
Q1-MAR-2002 (TrEMBLrel. 20, C;
01-MAR-2002 (TrEMBLrel. 20, Li
01-MAR-2004 (TrEMBLrel. 26, Li
Hypothetical protein.
                                                                                                        -----TEHSIPTP-
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992 KTKYTILDNMDEQERMELRP--KYGIKHRSTEHNSSLMVSESEFDSDQDTIFSREKMERG 1049
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SEQUENCE FROM N.A.

Oct T., Sulviki Y. Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sakine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Sakine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Sakine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Amamoto J., Sakine M., Morala M., Sudo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., An Abe K., Kandhara K., Yokoi T., Furuya T., Kikkawa E., Omura Y., An Ninomiya K., Ishibashi T., Yamashita H., Murakawa M., Yamazaki M., Anathana M., Watanabe S., Yosida M., Hotuta T., Kusano J., Anashita M., Maranabe S., Sono Y., Takahashi Fujii A., Hara H., Tanase T., Nomura Y., An Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Sano S., Noshikawa Y., Matsunawa H., Ichhara T., Shiohata N., Sano S., Noshikawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Amazaki M., Watanabe K., Kunagai A., Takemoto M., Suno S., Hishigaki H., Watanabe K., Kunagai A., Takemoto M., Suno Y., Shimizu F., Wakabata A., Takama A., Fujiwara T., Anno T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Okamoto S., Rawabata A., Hikiji T., Kobateke N., Inagaki H., Ikema Y., Okamata A., Hata H., Watanabe M., Komatau T., Shigeta K., Sanba T., Antsumara K., Nakajima Y., Matanabe M., Kohatau P., Nakagawa S., Sano J., Shima S., Komitani R., Rawakami T., Noguchi S., Itoh T., Shigeta K., Sanba T., Antsumara K., Nasajima Y., Matanabe M., Kakabatu J., Nakagawa K., Rakahashi T., Oyama M., Hata H., Watanabe M., Kakabahi Y., Namashita R., Namashita R., Namashita N., Kikuchi H., Matanabe M., Kakababata A., Wanashita R., Namashita M., Namashita M., Wanababata M., Namashita M., Kikuchi H., Noguchi S., Takhusu T., Nakagawa T., Nakagawa T., Nakagawa T., Nakagawa T., Nakagawa T., Nakagawa T., Nakagawa S., Sano S., Nama M., Hat
   DKELTLPVDSTTLDGSKSSDDQKIISYLWEKTQGPDGVQLENANSSVATVTGLQVGTYVF 362
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Hypothetical protein FLJ14225 (PKD1-like protein).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                    1004 QERMELRP--KYGIKHRSTEHNSSLMVSESEFDSDQDTIFSREXMERGNPKVSMNGSIRN 1061
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332 VKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGHKQ 391
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0RT-2004 (TrEMBLrel. 26, Last annotation update)
101-MR-2004 (TrEMBLrel. 26, Last annotation update)
11-MPOCHDETICAL protein DKFZp434C0829 (Fragment).
12-0RFZp434C0829;
13-0RFZp434C0829;
14-0RFZp434C0829;
15-0RFZp434C0829;
15-0R
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989 IRKKTKYTILDNMDEQERMELRP--KYGIKHRSTEHNSSLMVSESEFDSDQDTIFSREKM 1046
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                                                                                                                                                                                                                                                                         66 TISTVIDGSQSTDDDKIVQYHWEELKGPLREBKISEDTAILKLSKLVPGNYTFSLTVVDS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSEGGHVVMQCVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAV 628
  365 IVSYLWTRDEGSPAAGEVLNHSDHHPILFLSNLVEGTYTFHLKVTDAKGESDTDRTTVEV 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 HSQILKLSKLTPGLYEFKVIVEGGNAHGEGYVNVTVKPEPRKNRPPIAIVSPQFQEISLP
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                                             LISALIDGSQSTDDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNYSFRLTVTDS
                                                                                                                                              FYVOSRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Magage T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 8:85-95(2001).
EMBL. ABGSH40; BAB47466.1;
InterPro; IPR001961; FN III.
InterPro; IPR001961; FN III.
InterPro; IPR001961; FN III.
SMART; SM00060; FN3; 3.
SMART; SM00069; FN3; 4.
PROSITE; FS50093; FKD; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 2004; DB 2; Length 6; Pred. No. 3e-90; 82; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70427 MW; 0E8E348687170017 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            639 AA
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Name=KIAA1837;
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Matches 386; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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TISSUE=Brain;
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SEQUENCE
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Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A phykins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldow M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garchenko Y., Bouffauge S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffaud G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4,
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Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGT
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                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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TISSUB-Kidney;
Strausberg R.;
Strausberg R.;
Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK024287; BAB14874.1;
EMBL; AK024367; AAB131672.1;
EMBL; RO31672; AAB131672.1;
InterPro; IPR008957; FN III.
InterPro; IPR008957; FN III.
InterPro; IPR008657; FN III.
InterPro; IPR00869; FNJ; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.4%; Score 2086.5; DB 2; Length
60.7%; Pred. No. 3.1e-94;
.ive 88; Mismatches 173; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                      Genet. 36:40-45(2004)
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Matches 410; Conservative
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Gaps

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Length 639;

448

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Mus musculus (Mouse)
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Name=AU040320;
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STURBERS
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KEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KARAIN=EVBN/N; TISSUE=Liver;

KRIAUSER R.D., Feingold B.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B.B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Kichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rachey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                    YVFTLTVKDERNLQSQSSVNVIVKEEINKPPIAKITGNVVITLPTSTAELDGSKSSDDKG 365
                                                                                                                                                                                                                                                         QPDPRKSGLVELTLQVGVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIV 868
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SSKGKVVEMQGVRTPTLQLSAMQEGDYTYQLTVTDTIGQQATAQVTVIVQPENNKPPQAD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604
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                                                                                                                                                                                                                                IVSYLWIRDGOSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGASDTDTATVEV
                                                                                                                                                                                                                                                                                                                                                                                                                       FYVQSRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTK
                                           AGPDKELI PPVESATLDGSSSSDDHGI VPYHWEHVRGPSAVEMENI DKAI ATVTGLQVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
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STRAIN=FVB/N; TISSUE=Liver;
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993 TKYTILDNMDEQERMELRP--KYGIKHRSTEHNSSLMVSESEFDSDQDTIFSREKMERGN 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KELI PPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENI DKAIATVTGLQVGTYHFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRPPFKVLKAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTKRCIC
                                                                                                                                                                                                                                                                      513 NSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQIVLYEWSLGPGSEG
                                                                                                                                                                                                                                                                                                                                                    573 KHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVAGPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIVKDOQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIVSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LWIRDGOSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGASDTDTATVEVQPDP
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days embryo whole body cDNA, RIKEN full-length en
11brary, clone:C430042D23 product:HYPOTHETICAL 103.9 kDa PROTEIN
homolog (Fragment).
                                                                                                                                                                                                                                  5
                                                                                                                                                                                            DB 2; Length 603;
                                                                                                                                                      603 AA; 65967 MW; BE0DA1665D4046BD CRC64;
                                                                                                                                                                                                              ; Pred. No. 3.6e-74; 76; Mismatches 143;
MGD; MGI:2140475; AU040320.

GO; GO:0016020; C:membrane; IEA.
GO; GO:0001550; F:calcium ion binding; IEA.
GO; GO:0001156; P:nomophilic cell adhesion; IEA.
SMART; SM00060; FN3; 2.
SMART; SM00089; PKD; 3.
PROSITE; PSS0093; PKD; 1.
NON TER.
1 1 1
SEQUENCE 603 AA; 65967 MW; BEODA1665D4046BD
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Matches 328; Conservative
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SEQUENCE FROM N.A.
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YPPVANAGPNHTITLPQNSITLNGNQSSDDHQIVLYEWSLGPGSBGKHVVMQGVQTPYLH 586
                                                                  70 AWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGI 129
                                                                                                                                                                                    130 WGDSPEDIRKDLXFLGKDWGLEE-------MSEYXDDYRELEKDLLQPSGKQEPR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                 231 ERSVLLPLPTTPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKS 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 SYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVD 526
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                                                                                                                                                                                                                                                                                                                                                                     187 --RQKRDLSVVPTHGAMQHSKVNHSEEAGALSPTSAEVRKTITVAGSFTSNHTTQTPEWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNVSIHPEPS----BHSSPVSG-----BHSSPVSG-----
                                                                                                                                                                                                                          98 LWWLEGMCFQADCSKPQSCQPFRTDSSNSML-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUB=Whole body;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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STRAINS-25913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=2059013; PubMed=11076861; DOI=10.1101/gr.152600;
A MEDLINE=2059013; PubMed=11076861; DOI=10.1101/gr.152600;
A Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakquchi S., Ikagami T., Kashiwagi K., A Yanamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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STRANS=CSTBAL,61; TISSUE=Whole body;
STRANTOM CONSOCTIUM,
THE FANTOM CONSOCTIUM,
THE RIKEN GENOME Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
Nature 420:563-573(2002).
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STRANIE-SCYBL/6J; TISSUE-Whole body;
MEDILINE-21.085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
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PROSITE; PS50093; PKD; 1.
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SEQUENCE FROM N.A.
MEDILINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                       PRT; 1069 AA
                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
                                                                                                       PRELIMINARY;
VNV 682
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Ballew R.M., Baua A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
Beason K.Y., Benos P.V., Berman B.P., Bhandari D., Bolbhakov S.M.,
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
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MEDLINE=22426070; PubMed=12537573;
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to the EMBL/GenBank/DDBJ databases

Submitted (SEP-2002)

FlyBase

SEQUENCE FROM N.A

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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)

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                                                                                                                            .01186; EGF 2; UNKNOWN 1.
1069 AA; 117310 MW; ZBA50A62EEE463DB CRC64;
             the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      ilarity 32.1%; Pred. No. 7.5e-63;
Conservative 172; Mismatches 383;
                      EWBL, AE003556; AAF50494.1; --
FlyBase; FBGR0035833; CG7565.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
SMART; SM00181; EGF; 1.
                                                                                                                            PROSITE; PS01186; EGF
FlyBase;
Submitted (MAR-2004)
                                                                                                                                                                                    Best Local Similarity
Matches 373; Conserv
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Search completed: October 12, 2005, 10:21:38 Job time : 134 Becs

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; Search time 908 Seconds (without alignments) 491.154 Million cell updates/sec
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2. (cgn2 6/prodate 2/pubpaa/USO7 NEW PUB. pep:*
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Sequence 3, Appli Sequence 5, Appli Sequence 9, Appli Sequence 12, Appl Sequence 259, App Sequence 273, App Sequence 274, App Sequence 7, Appli Sequence 1622, Ap Sequence 11, App. Description US-10-408-765A-1622 US-10-764-390-11 US-10-764-390-3 US-10-764-390-8 US-10-764-390-9 US-10-764-390-2 US-10-764-390-259 US-10-764-390-273 US-10-764-390-274 US-10-764-390-274 G Length DB 1072 1072 1072 1072 1072 1072 1072 1053 Query Match 1 99 9.66 9.69 Score

Sequence 10, Appl Sequence 272, App	16	Sequence 39353, A	Sequence 175, App	Sequence 175, App	Sequence 49627, A	Sequence 110, App	'n	Sequence 133, App	~	4	11,	20,	155	1224	751,	Sequence 31983, A	Sequence 37319, A	24	126	21,	18,	22,	4	Š	9	4	5426	Sequence 5, Appli	4616	46577		5784,
US-10-764-390-10 US-10-764-390-272	US-11-097-143-168	US-10		US-10	US-10	US-10-805-684-11	US-09-759-508B-2	US-10	US-10	US-10	/ US-10-875-518-11	US-10	3 US-10-840-512-155	US-11-097-143-12		US-11-097-143-319	US-09-864-761-37319	US-10-029-386-324	US-09-989-442-126	US-10	US-10-470-390A	US-10	S US-10-203-875-4	US-10-29	US-10-369-493-1023	US-10-45	ns	US-10-41	US-10-282	US-10-282-122A-	US-09-840-7	3 US-10-369-493-5784
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ALIGNMENTS

1 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA 1 MAPPIGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA Gaps Sequence 1622, Application US/10408765A
; Sequence 1622, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Zhang, Bing
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Bradford W.
APPLICANT: Glenn, Gary M.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF ENVENTION WINBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1622
; LENGTH: 1072 ö Length 1072; Indels 3; DB 16; Score 5576; DE Pred. No. 0; 0; Mismatches 99.98; Conservative ; ORGANISM: Homo sapiens US-10-408-765A-1622 Similarity Query Match Best Local Simil Matches 1069; C

61 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 120

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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao

APPLICANT: Ge, Wangmao

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

APPLICANT: Duan J. Perez-Villar

ITILE OF INVENTION: Entiled 254Plb6B Useful in Treatment and Detection of

ITILE OF INVENTION: Entiled 254Plb6B Useful in Treatment and Detection of

ITILE OF INVENTION: Entiled 254Plb6B Useful in Treatment and Detection of

CURRENT APPLICATION NUMBER: US/10/764,390

CURRENT APPLICATION NUMBER: US/04-01-23

FRIOR APPLICATION NUMBER: US/04-01-23

FRIOR APPLICATION NUMBER: US/04/41,526

PRIOR PRILING DATE: 2003-01-24

NUMBER OF SEQ ID NOS: 277

SSQ ID NO 11

INDUMBER OF SEQ ID NOS: 277

SSQ ID NO 11

INDUMBER OF SEQ ID NOS: 277

INDUMBER OF SEQ ID NOS: 277

SSQ ID NO 11

INDUMBER OF SEQ ID NOS: 277
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ive 0; Mismatches
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CRGANISM: Homo sapiens
US-10-764-390-11
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SULT 2 :10-764-390-11 Sequence 11, Application US/10764390 Publication No. US20040214212A1 GENERAL INFORMATION:

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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Baitano, Arthur B.
APPLICANT: Jakbovits, Aya
APPLICANT: Jakbovits, Aya
APPLICANT: Gallita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US6/442,526
PRIOR APPLICATION NUMBER: US6/442,526
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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; Sequence 8, Application US/10764390
; Publication No. US20040214212A1
; GENERAL INFORMATION:
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Best Local Similarity 99.77
Matches 1069; Conservative
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US-10-764-390-8
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APPLICANT: Agensys.

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APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Ge, Wangmao

APPLICANT: Ge, Wangmao

APPLICANT: Steven B. Kanner

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                                                 Sequence 5, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
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Matches 1069; Conservative
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ORGANISM: Homo sapiens
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Corresponding Proteins
Useful in Treatment and Detection of
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APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Feris, Mary
APPLICANT: Feris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Entitled 254PlD6B Usefu;
TITLE OF INVENTION: Entitled 254PlD6B Usefu;
TITLE OF INVENTION: Entitled 254PlD6B Usefu;
TITLE OF INVENTION: Entitled 254PlD6B Usefu;
TITLE OF INVENTION: Cancer:
FILE REFERENCE: 51158-20081.0
CURRENT APPLICATION NUMBER: US60/442,526
PRIOR APPLICATION NUMBER: US60/442,526
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SEQ ID NOS: 277
SEQ ID NOS: 277
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.7%;
Matches 1069; Conservative 0
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ORGANISM: Homo sapiens
US-10-764-390-9
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Sequence 9, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION: APPLICANT: Agensys, Inc.; APPLICANT: Raitano, Arthur B. RESULT 6 US-10-764-390-9

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EHVRGPSAVEMENI DKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKGENNSPPR

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                                                                                                                  EHSIPTTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP
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                                      TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST
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Publication No. US20040214212A1
GENERAL INFORMATION:
APPLICANT: Agensy, Inc.
APPLICANT: Gaitano, Arthur B.
APPLICANT: Gaitano, Arthur B.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-villar
APPLICANT: Juan J. Perez-villar
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APPLICANT: Nucleic Acids and Corresponding Proteins
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US-10-764-390-12

i Sequence 12, Application US/10764390

j Publication No. US20040214212A1

GENERAL INFORMATION:

j APPLICANT: Raitano, Arthur B.

APPLICANT: Raitano, Arthur B.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Ge, Wangmao

APPLICANT: Steven B. Kanner

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Pred. No. 0;
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Best Local Similarity 99.7%;
Matches 1069; Conservative
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ORGANISM: Homo sapiens
US-10-764-390-12
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Matches 1050; Conservative
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US-10-764-390-273
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TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of ITLE OF INVENTION: Cancer FILE REFERENCE: 51188-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US60/442,526
PRIOR PELING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE PRESER FRESEQ for Windows Version 4.0
SEQ ID NO 259
LENGTH: 1072
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Pred. No. 0;
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Matches 1069; Conservative
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GENERAL INCORANTIANS

APPLICANT: Agensys, Inc.

APPLICANT: Raitano, Arthur B.

APPLICANT: Taitano, Arthur B.

APPLICANT: Taitano, Arthur B.

APPLICANT: Taitano, Arthur B.

APPLICANT: Ge, Wangmao

APPLICANT: Faris, Mary

APPLICANT: Faris, Mary

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APPLICANT: Brish, Mary

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APPLICANT: Brish, Mary

TITLE OF INVENTION: Entitled 254PlD68 Useful in Treatment and Detection of

TITLE OF INVENTION: Entitled 254PlD68 Useful in Treatment and Detection of

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE APPLICATION NUMBER: US60/442,526

PRIOR FILING DATE: 2004-01-23

PRIOR FILING DATE: 2003-01-24

NUMBER OF SEQ ID NOS: 277

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 273

TENNOTH 105.1 1020 840 960 199 180 240 319 300 900 80 VSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK 139 120 259 ELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPT 379 4 9 901 LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLMMENLIQRYIWDGESNCEWSIFYVT VSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRK DLPFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV GDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTPSSGEVLEKEKASQLQEQ 241 SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPS VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1 CARKQCSEGRIYSNAVISPNLETIRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL 140 DLXFLGXDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSV SSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPATSAAPSESTPS LAVLLINVLDSDI KVQKI RAHSDLSTVI VFYVQSRPPFKVLKAAEVARNLHMRLSKEKADF LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT 20 CARKOCSEGRIYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYL GDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQ EHNSSLAVSESEPDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072 ö Length 1053; Indels DB 16; 3; Score 5485; DB Pred. No. 0; 0; Mismatches

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                       PQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNY
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                                                               SFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQI
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US-10-764-390-274
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 274
LENGTH: 1053
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
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APPLICANT: Gainsys, Inc.
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Uncleic Acids and Corresponding Proteins
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Sequence 10, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
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99.7%; Pred. No. 0;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 7, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION:
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Matches 1050; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Agensys, Inc.
APPLICANT: Jakobovits, Aya
APPLICANT: Gaboovits, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
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Pred. No. 0;
0; Mismatches
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1040 IFSREKMERGNPKVSMNGSIRNGASFSYCSKDR
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                                                                     RESULT 13
US-10-764-390-272
US-10-764-390-272
Sequence 272, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
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Best Local Similarity 99.7
Matches 1050; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-390-272
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            Query Match 98.3%; Score 5485; D
Best Local Similarity 99.7%; Pred. No. 0;
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC;
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC;
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC;
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO00728
CURRENT APPLICATION NUMBER: 60/157, 832
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR PILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 2000-01-2
PRIOR PILING DATE: 2000-01-2
PRIOR PILING DATE: 2000-02-2
PRIOR APPLICATION NUMBER: 60/194,831
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Publication No. US20050208558A1
GENERAL INFORMATION:
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ORGANISM: DROSOPHILA
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Query Match 26.0%; Score 1451.5; DB 20; Length 1069; Best Local Similarity 32.1%; Pred. No. 2.3e-80; Matches 373; Conservative 172; Mismatches 383; Indels 233; Gaps
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764 GDVIDGSDHSVALQLINLVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 PONSITLINGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKV 601
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                  DPLTKRCICSHLWMENLIQRYIWDG-ESNCEWSIFYVTVLAFTLIVLTGGFTWLCICCCK
                                                             ROKRIKIRKKT-KYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDTIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 711;
                                                                                                                                                                                                                                    ; Sequence 39353, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; FILE BERERENCE: 790C1P3/US;
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; PRIOR PLICATION NUMBER: 09/649,167
; RIOR APPLICATION NUMBER: 09/649,167
; NUMBER OF SEQ ID NOS: 60736
; SEQ ID NO 39353
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COTHER INFORMATION: Xaa = X or * as defined in Table
US-10-450-763-39353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.6%; Score 1375; DB 18; Best Local Similarity 48.4%; Pred. No. 6.7e-76; Matches 358; Conservative 43; Mismatches 172;
                                                                                   1042 SREKMERGNPKVSMNGSIRNG 1062
                                                                                                                                                     ETRIKSNGLGKHKSHNSHSHG 1041
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ORGANISM: Homo sapiens
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345 QDVIDGSDHSVALQLTNLVEGVYTFHFLMLXSLCKCPSANPVSSLSPDPRKSGLVELTLQ
                                    824 VGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDL-STVIVFYVQSRPPFKVLKA
                                                                                                                                                                  942 QRYIWDGESNC--EWSIFYVTVLAFTLIVLTGGFTWLCI-----CCCKRQKRTKIRKKT-
                                                                                                                                                                                                                                                                                           1024 SSLMVSESEFDSDQDTIFS 1042
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completed: October 12, 2005, 10:18:07 e : 913 secs

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APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
                                                                                   SUMMARIES
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-Q=/Cgn2 1/USPTO spool p/US10764390/runat 12102005_110204_22383/app_query.fasta_1.1223
-Q=/Cgn2 1/USPTO spool p/US10764390/runat 12102005_110204_22383/app_query.fasta_1.1223
-Q=/Cgn2 1/USPTO spool p/US10764390/runat -LEND=1.mpb-numATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=b1ts -START=1 -END=-1 -MATRIX=b1osum6.
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100
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(without alignments)
1960.176 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                  OM protein - nucleic search, using frame_plus_p2n model
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
FRIOR APPLICATION NUMBER: US60/442,526
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 6791
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NAME/KEY: misc feature
LOCATION: (0)...(0)
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FEATURE: OTHER INFORMATION: Pos: 5641; r = g or a	0-764-390-3 (1-1072) x US-10-764-390-2 (1-6791)	1 MetAlaProProThrGlyValLeuSerSerLeuLeuLeuLeuValThrIleAlaGlyCys 20 	21 AlaArgLysGlnCysSerGluGlyArgThrTyrSerAsnAlaValIleSerProAsnLeu 40 	41 GluThrThrArgIleWetArgValSerHisThrPheProValValAspCysThrAlaAla 60 	61 CysCysAspLeuSerSerCysAspLeualaTrpTrpPheGluGlyArgCysTyrLeuVal 80 	81 SerCysProHisLysGluAsnCysGluProLysLysNetGlyProIleArgSsrTyrLeu 100 	101 ThrPheValLeuargProValGlnArgProAlaGlnLeuLeuaspTyrGlyAspWetMet 120 	121 LeuasnargGlySerProSerGlyIleTrpGlyAspSerProGluAspIleArgLysAsp 140 	141 Leu***PheLeuGlyLysAspTrpGlyLeuGluGluMetSerGluTyr***AspAspTyr 160 	161 ArgGluLeuGluLysAspLeuLeuGlnProSerGlyLysGlnGluProArgGlySerAla 180 	181 GluTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsnSerValGly 200	201 AspSerProAlaValProAlaGluThrGlnGlnAspProGluLeuHisTyrLeuAsnGlu 220 	221 SerAlaSerThrProAlaProLysLeuProGluArgSerValLeuLeuProLeuProThr 240	241 ThrProSerSerGlyGluValLeuGluLysGluLysAlaSerGlnLeuGlnGluGluGlnSer 260
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1312 AACAATAGACCTCCAGTGGCTGGCCCCTGATAAAGAGCTGATCTTCCCAGTGGAA 2431 2432 AGTGCTACCCTGGATGGCAGCAGCACCCCTGATAAAGAGCTGATCTTCTACCACTGG 2491 2432 AGTGCTACCCTGGATGGCAGCAGCAGCAGCACTTCACCACTGG 2491 2432 AGTGCTACCCTGGATGGCAGCAGCAGCAGCACTTCTCTTCTACCACTGG 2491 2492 GAGCACGTCAGAGGCAGCAGCAGCAGCAGCACTTCACCACTGG 2491 2492 GAGCACGTCAGAGGCAGCAGCAGCAGCAGCAATATTCACAAAACAATAGCCACT 2555 2401 HILLIAN HI	3272 GGTCGCGCCCCCCCCCCTCGCTTTGCTCTCTTTTGGTGTGGTG
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Db 3452 TGCAAAAGACAAAAAGGACTAAAATCAGGAAAAAACAAAGTACACCATCCTGGATAAC 3511 Qy 1001 MetaspGluGlnGluArgMetGluLeuArgProLysTyrGlyIleLysHisArgSerThr 1020	RESULT 2 1. Sequence 4, Application US/10764390 1. Sequence 4, Application US/10764390 2. Sequence 4, Application US/10764390 3. Publication No. US20040214212A1 CENERAL INFORMATION: 3. APPLICANT: Raitano, Arthur B. 4. APPLICANT: Raitano, Arthur B. 4. APPLICANT: Raitano, Arthur B. 5. APPLICANT: Ga, Wangmao 5. APPLICANT: Ga, Wangmao 5. APPLICANT: Ga, Wangmao 6. Wangmao 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 7. APPLICANT: Steven B. Kanner 8. PRICA PRICA PRICA STOR NUMBER: US60/442,526 PRICA PRICA PRICA STOR NOW STOR STOR STOR STOR STOR STOR STOR STOR	Alignment Scores:

Cy 801 ThrAspThrAlaThrValGluValGlnProAspProArgLysSerGlyLeuValGluLeu 820	821 ThrLeuGlnValGlyValGlyGlnLeuThrGluGlnArgLy8AspThrLeuValArgGln 8	Qy 841 LeualaValLeuleuAsnValLeuAspSerAspIleLysValGlnLysIleArgAlaHis 860	Qy 861 SerAspLeuSerThrVallleValPheTyrValGlnSerArgProProPheLygValLeu 880	881 LysAlaAlaGluValAlaArgAsnLeuHisMetArgLeuSerLysGluLysAlaAspPhe 	901 LeuleuPheLysValleuArgValAspThrAlaGJyCysLeuleuLysCysSerGlyHis 	921 GJyHisCysAspProLeuThrLysArgCysIleCysSerHisLeuTrpMetGluAshLeu 	IleGirakgTv11eTrpAspGlyGiuSerAanCysGluTrpSerIlePheTyrValThr 	961 ValleuAlaPheThrLeuIleValLeuThrGlyGlyPheThrTrpLeuCysIleCysCys	981 CyslysArgGlnLysArgThrLys1leArgLysLysThrLysTyrThr1leLeuAspAsn 	Oy 1001 MetAspGluGinGluArgMetGluLevArgProLysTyrGlyIleLyeH1sArgSerThr 1020 	Qy 1021 GluHisAsnSerSerLeuMetValSerGluSerGluPheAspSerAspGlnAspThrIle 1040	Oy 1041 PheSerargGluLysMetGluArgGlyAsnProLysValSerMetAsnGlySerIleArg 1060 [Qy 1061 AsnGlyalaSerPheSerTyrCysSerLysAspArg 1072 	RESULT 3 US-10-764-390-270 ; Sequence 270, Application US/10764390 ; Publication No. US20040214212A1	GENERAL INFORMATION: APPLICANT: Agensys, Inc. APPLICANT: Rattano, Arthur B. APPLICANT: Gakobovits, Aya	; AFPLICANT: Ge, Wangmao; APPLICANT: Ge, Wangmao; APPLICANT: Faris, Mary; APPLICANT: Fare, Mary; APPLICANT: Steven B. Kanner;	 APPLICANY: Juan J. Perez-Villar TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of TITLE OF INVENTION: Cancer
AATGTCACTGTTAAGCCTGCCAGAAGAGTCAACCTGCCACCTGTAGCAGTTGTTT GInLeuGInGluLeuThrLeuProLeuThrSerAlaLeuIleAspGlySerGInS 	CAACTGCAAGAGCTCACTTTGCCTTTTGACGTCAGCCCTCATTGATGGCAGCCAAAGTACAAASPABPThrGlu11eValSetTyrHieTrpGluGlu11eAsnGlyProPhelleGluGlu	1892 GATGATACTGAAATAGTTATCATTGGGAAGAATAAACGGGCCTTCATAGAAGAG 1951 481 LysThrSerValaspSerProValLeuargLeuSerAsnLeuaspProGlyAsnTyrSer 500 1952 AAGACTTCAGTTGACTCTCCCGTCTTATCTTAACCTTGATCCTGGTAACTATAGT 2011	PheArgLeuThrValThrAspSerAspGlyAlaThrAsnSerThrThrAlaAlaL 	ValasnasnalavalaspTyrProProValalaasnalaGlyProAsnHisThrIleThr 	541 LeuproGlnAenSerlleThrLeuAenGlyAenGlnSerSerAepAspHisGlnIleVal 560 	561 LeutyrGlutrpSerLeuGlyProGlySerGluGlyLyBHisValValMetGlnGlyVal 580 	581 GlnThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAspTyrThrPheGlnLeuLys 600 	601 ValThraspSerSerArgGlnGlnSerThrala***ValThrValIleValGlnProGlu 620 	621 AsnAsnargProProValaladayProAspLysGluLeuIlePheProValGlu 640 	641 SeralaThrLeuAspGlySerSerSerSerapaspHisGlyIleValPheTyrHisTrp 660 	GlubisvalArgGlybroserAlavalGluberGlubsnileAspLysAlaileAlaThr 	ValThrGlyLeuGlnValGlyThrTyrHisPheArgLeuThrValLysAspGlnGly 	LeuSerSerThrSerThrLeuThrValAlaValLysLysGluAsnAsnSerProProArg	721 AlaargaladiydiyarghisyalLeuvalLeuproasnasnSerileThrLeuAspGly 740 	741 SerargSerThraspaspGlnargIleValSerTyrLeuTrpIleArgAspGlyGlnSer 760 	761 ProAlaAlaGlyAspVall1eAspGlySerAspHisSerValAlaLeuGlnLeuThrAsn 780 	781 LeuValGluGlyValTyrThrPheHisLeuArgValThrAspSerGlnGlyAlaSerAsp 800

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Matches:
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FILE REFERENCE: S1158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
FRIOR APPLICATION NUMBER: US60/442,526
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 270
LENGTH: 6797
                                                                                                                                                                  Gaps:
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5546.50
99.53%
99.53%
20.40%
                                                                            TYPE: DNA
CRGANISM: Homo sapiens
US-10-764-390-270
                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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JURENTAL INCRAFACE

JAPPLICANT: Raitano, Arthur B.

APPLICANT: Raitano, Arthur B.

APPLICANT: Raitano, Arthur B.

APPLICANT: Talita-Eid, Pia M.

APPLICANT: Ge, Wangmao

APPLICANT: Faris, Mary

APPLICANT: Faris, Mary

APPLICANT: Faris, Mary

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins

TITLE OF INVENTION: Raitled 254P1D6B Useful in Treatment and Detection of

TITLE OF INVENTION: Cancer

FILE REFERENCE: 51158-20081.00

CURRENT FILING DATE: 2004-01-23

PRIOR PAPLICATION NUMBER: US60/442,526

NUMBER OF SEQ ID NOS: 277

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 271

LENGTH: 6797
                                                        3573
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                                                                                                                                                                                           RESULT 4
US-10-764-390-271
US-10-764-390-271
, Sequence 271, Application US/10764390
, Publication No. US20040214212A1
, GENERAL INFORMATION:
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US-10-764-390-271
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Best Local Similarity:
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                                                          GGAAAGTGCTACCCTGGATGGGAGCAGCAGCAGCGATGACCACGCCATTGTCTTCTACCA
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4 CGCTTGCTGTGACCTGTCGACCTGGCCTGGTGGTTCGAGGCCGCTGCTACCT 75 9 uValSerCysProHisLysGluAsnCysGluProLysLysNetGlyProIleArgSerTy 99	874 GATGCTGAACAGGGGCTCCCCCTCGGGGGAATCTCACCTGAGGATATCAGAAA 933 139 SASDLeu***PheLeuGlyLysAsDTrpGlyLeuGluGluMetSerGluTyr***AspAs 159 130 GASTGCCCTTTTAGGCAAGATTGGGGCCTTGAGGAGTATCAGATATCAGTACTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTA	1054 TGCCGAGTACACGGACTACTGCCGGCGAGGGGGCCTTCAACTCCTCTGT 1113 199 1G1yAspSerProAlaVa1ProAlaG1uThrG1nG1nAspProG1uLeuHisTyrLeuAs 219 1114 TGGAGACAGTCCTGCGGTGCCAGCGGAGCGAGCAGCAGCAGCAGCTCCTTACCTGA 1173 219 1G1\Section	GACTACTCCATCTTCAGGAGAGGGTGTTGGAGAAAAGACTTCTCAGCTCCAGGAACA INSERSEARANSELSETGIJLYSGIUVALLEUWELPROSETHISSETLEUPROPROALASE	1414 TACAGAGCACCACCACCACCACTAGCGCAGCCCCTCTGAGTCCACCCCATC 1473 319 rGluLeuProlleSerProThrThralaProArgThrValLysGluLeuThrValSerAl 339 1474 TGAGCTACCCATTCTCTCTACCACTGCTCCAGGACGTGAAAGAACTTACGGTATCGGC 1533 339 aGlyAspAsnLeuIlelleThrLeuProAspAsnGluValGluLeuLysAlaPheValAl 359	1594 GCCAGCGCCACCTGTAGAAACAACCTAAACTATGAATTTAATAAGCCACCCAC

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| Sequence 6, Application WS/10764390
| Publication No. US20040214212A1
| GENERAL INFORMATION:
| APPLICANT: Raitano, Arthur B. |
| APPLICANT: Challita-Eid, Pia M. |
| APPLICANT: Challita-Eid, Pia M. |
| APPLICANT: Steven B. Kanner |
| APPLICANT: Steven B. Kanner |
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CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US60/442,526
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: PASLSEQ for Windows Version 4.0
LENGTH: 6991
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APPLICANT: Abdobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
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TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Gancer
FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US6/442,526
FRIOR FILING DATE: 2004-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 269
LENGTH: 6991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 269, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION:
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US-10-764-390-269
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                                                                                                                      -------GlnArgProAlaGlnLeuLeuAspTyrGlyAsp 118
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MetGlyProlleArgSerTyrLeuThrPheValLeuArgProVal--------
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APPLICANT: Venter, J. Craig
APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 06/157,832
PRIOR RILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-110-28
PRIOR FILING DATE: 1999-110-28
PRIOR FILING DATE: 1999-110-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/194,831
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SEQ ID NO 16883
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Publication No. US20050208558A1
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
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                                                                                                                                                                                                                           LOCATION: (479)..(1723)
COTHER INFORMATION: 60% homologous to Homo sapiens dJ73M23.3 (KIAA0319), accession
CHER INFORMATION: number AL031230, Smith-Waterman Score=1025.

SCORE 1025.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleLysGlnGlyHisLysGlnThrLeuAsnLeuSerGlnLeuSerValGlyLeuTyrVal
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CTTGCATGTTGAACTGTACAACTTTTTCTTTATGTTACAGTTGTCCGTCGGACTTTATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTTTTTTTTTACAGCCAGAAGAGTCAACCTGCCACCTGTAGCAGTTATAAAACTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTCCTCTTGTATTTCATTCTTGTCTTTATTCTTAATCTTGTAGAAAGTACAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnAsnAlaValAspTyrProProValAlaAsnAlaGlyProAsnHisThrIleThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProGlnAsnSerIleThrLeuAsnGlyAsnGlnSerSerAspAspHisGlnIleValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 TTGTTTTGTTTT----------
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358
41
164
188
23
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FLING DATE: 2000-03-31
PRIOR FLING DATE: 2000-03-31
PRIOR FLING DATE: 2000-03-31
PRIOR FLING DATE: 2000-03-31
PRIOR FLING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CLUSCOM
SEQ ID NO 8985
LENGTH: 2423
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1314.00
53.20%
47.73%
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                               NAME/KEY: SIMILAR
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Pred. No.:
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Alignment Scores: Pred. No.: Pred. No.: Score: Score: Fercent Similarity: Best Local Similarity: Conservative: Description: Best Local Similarity: 24.95\$ DB: Conservative: Alignatches: Al	US-10-764-390-3 (1-1072) x US-11-097-143-16882 (1-5775) Qy	Db 1157 ATTGCAACCTGCTTTTGCTGGCCACTGCGATGTCGTCAGCATATGCCGACGTCAACG 1216 Qy 22ArgLysGlnCysSerGluGlyArgThrTyr 31	Db 1217 CAAAACGCTCTGTTGGAAGTAAGAAACACAAGGAGACCAGCCCCGATAATTCAGTT 1276 Qy 32 SerAsnalaValileSerProAsnLeuGluThrThrArgileMetArgValSerHisThr 51	:::	OY 52 PhePro 53	Oy 54 ValValAspCysThrAlaAla 60	Db 1388 CCGCCGGATGCAGTGGAGCCACTGGAGGAGGCCTATCTTTGGAACTGCCTACAGGCT 1447 Ov 61 CYBCYSARD	::: 1448 TGCTGCGAAAAGCCCCGGAATGGCAGCAGTGCCTG	Oy 76 ArgCysTyrLeuValSerCysProHisLysGluAsnCysGluProLysLys 92	Qy 93 MetGlyProlleArgSerTyrLeuThrPheValLeuArgProVal 107	CCACA	119 MetMetLeudsnargGlySerProSerGlyIleTrpGlyAspSerProGluAspIleArg	Qy 139 Lysabgleu***PheLeuGlyLysasp	Oy 152GluMetSerGluMetSerGluTyr***AspAsp 159	160TyrArgGluLeuGluLysAspLeuLeuGlnProSerGlyLysGln	Db 1832 GATTTCCCATTGGCCGACAAGCGAATGAATCAAATGATCTTCCAACCGACGAAAAC 1888	Qy 175 GluProArgGlySerAlaGluTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAla 194	Db 1888 1888	Qy 195 PheAsnSerSerValGlyAspSerProAlaValProAlaGluThrGlnGlnAspProGlu 214	Qy 215 LeuHisTyrLeuAsnGluSerAlaSerThrProAlaPro 227 ::: ::
QY 922 SCYSASPPROLEUThruySARGCYSIIe CYGSSET 933 Db 1510 CTGCGACCCCTCACAAAGCGCTGCATTTGAAAATAAAGTTGTTCTACAAATAGCCTGTA 1569 QY 934HisLeuTpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluGerAs 951 Db 1570 ACTATGTCCACTTGGTTT 1:	Qy 951 nCysGlutrpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLe 969 	Qy 969 uThrGlyGlyPheThrTrpLeuCysIleCysCysCysLysArgGl 984	Qy 984 nLysargThrLysIleargLysLysThr	Qy 996 ThrileLeuAsp 999	Db 1756 TACCCATTGAATTCTAATCCTGCCCATAGCGGTACGAGGTATGTGCAATGATTATCCCCA 1815 Qy 1000AsnMetAspGluGlnGluArgMetGluLeuArgProLysTy 1013	1816 CGACTGACAGCTGGAAG	Qy 1013 rGlylleLysHisArgSerThrGluHisAsnSerSerLeuMetValSerGluSerGluPh 1033	eAspSerAspGlnAspThrIlePheser 1042	Db 1936 GAGTTTTGACAGGGACTGTGCAAAGC 1963 RESULT 9	US-11-097-143-16882 ; Sequence 16882. ; Publication No. US20050208558A1 ; GENERAL INFORMATION:	; APPLICANT: Venter, J. Craig ; APPLICANT: et al. ; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID ; TITLE OF INVENTION: APPAYS FOR DETECTING EXPRESSION OF 10,000 OF MORE	NES.	APPLICATION NUMBER: 60/157,83 FILING DATE: 1999-10-05 APPLICATION NUMBER: 60/160,19 FILING DATE: 1999-10-19	; PRIOR APPLICATION NUMBER: 60/161,932 ; PRIOR FILING DATE: 1999-10-28 ; PRIOR PRIFING DATE: 1999-11-12		; PRIOR APPLICATION NUMBER: 60/175,693 ; PRIOR FILING DATE: 5000-01-12. ; PRIOR APPLICATION NUMBER- 60/184 831	FILING DATE: 2000-02 APPLICATION NUMBER:	FILING DATE: 2000-0.	RE: FastSEQ for 40 16882 1: 5775	; TYPE: DNA ; ORGANISM: DROSOPHILA US-11-097-143-16882

Qy 567 GlyProGlySerGluGlyJ Db 2891 GATGTAGCGAGGCCG Qy 587 LeuSeralaMetGlnGluGluG Db 2951 CTGTCAATTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	633 3131 648 3190 667 673 3310	Oy 588 INT. THISPERSAGED ON 588 INT. THISPERSAGED ON 3370 CTCTARGAGTTGAATTA OY 708 ThrValalaValLySLyS. Oy 714	Db 3609 CTGGCTGTGGTCAAGTAT Oy 767 11eAepGlySerAepHisi 15.
1910 CTCGGCTACTACGATTCGAATGCCAAGTTTACCACCTGCGATATGGAGACACCTTGTCCA 1969 228 LysleuProGluArgSerValLeuLeuProLeuProThrThrProSerSer	ovalLeuThrValThrProGlySerThrGluHisSerIleProThrProProThr	369 AsnTyrGluTrpAsnLeulleSerHisProThrAspTyrGluGlyGluIleLysGln 387 2291 AAATATCTTTGGACACTTATATCGCAACCCAAGGCTCCTATGAATTTCGGAT 2350 388 GlyHisLysGlnThrLeuAsnLeuSerGlnLeuSerValGlyLeuTyrValPheLysVal 407 381 CAGAGCAAGTCGAAGGTAAAACTATCGAATCTTTCGGAGGGACTGTATACTTTTAAGGTC 2410 408 ThrValSerSerGluAsnAlaPheGlyGluGlyPheValAsnValThrValLysPro 426 411 ACTGTAACTGGTGAATGGAAGCTTTGGCGAGGGAACTGTATACTTTTTAAGGTC 2410 427 AlaArgAAGTGAATGGAAGCTTTGGCGAGGCAACACGTTAAAGTGCTTCCC 2470 427 AlaArgAAGTGAATGGAACCTTTGGCGAGGCAACAGCCAATGTTACAGTGCTTCCC 2470 427 AlaArgAATGGAATCGAATGGAAGCCAATGATGATCATCTCCC 2470 427 AlaArgAATGAATGAATGGAACCTTTGGCGAGGCAACAGCCAAGGAATCATCCGT 2530 447 LeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThrAspAspAspThrGluileVal 466	2531 CAGCCCACCATGCTATGGCAGCAGCAGTACGATGAGATGACC 2590 467 SerTyrHisTrpGluGlulleAsnGlyProPhelleGluGluLysThrSerValAspSer 486 5::::
8 6 8 6 8 6 8 8	8 4 8 4 8 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8 8 8 8 8 8 8	8 6 8 6 8 6 8 6 8

*ValThrValIleValGlnProGluAsnAsnArgProProVal 626 BGIYILEVAlPheTYRH18TrpGluH18VAlArgGlyPro--- 666 ||| |||::: ||| ||| |||||||||| 3548 OASDASDSEIleThrLeudapGlySerArgSerThrAspAsp 746 ||ThraspserginglyalaserAspThraspThralaThrval 806 ||:::||| |||||| |:: ::|||||| |||||| |GagcgaTgaTcAgGGTTTGACCAGTTCAGATACTGTCAGCGTT 3847 nArgiysAspThrLeuValArgGInLeuAlaValLeuLeuAsn 846 YLYBHİBVALVALMETGINGLYVALGINTKEPFOTYFLEUHİB 586 ||| ||| ||| |||||| |CAAGGCTGTGGATATGCAGAATACAAGAACACCCTATGTTCAG 2950 GGCATGTACACTTTTGTTCTAAAAGTAACCGATGGCAGTGGG 3010 PACGGTAGGTTTCAGTTAAAAGATTATTTTTTTTTTAA 3130 AAGGTAATCATATCCATAATCTTCAGTAGCTCATAGGTGCTAA 3488 |||||||| ||||||| ::: TCTCTGGACACGCGACGACACTTTGGCAGCGGCGTCATT 3668 ----ValAlaLeuGlnLeuThrAsnLeuValGluGlyValTyr 786 GTCCAACTCATCAGTAAGTGCATATATATATATCGTTATGTTG 3309 -GGAGCCCGTAATGATTGTGAGTTAAGATTTAACTCTAATCCC 3727 JGlyAspTyrThrPheGlnLeuLysValThrAspSerSerArg 606 nileAspLysAlaileAlaThrValThrGlyLeuGlnValGly 687 urhrvallysAspGlnGlnGlyLeuSerSerThrSerThrLeu 707 ----GludsndenSerProProArgaladrgalaglyGlyArg 726 rrLeuTrpIleArgAspGlyGlnSerProAlaAlaGlyAspVal 766 8Ser----- 773 OArgLysSerGlyLeuValGluLeuThrLeuGlnValGlyVal 826

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AGCAGCACGTCCACCTCACTGTGGCTGTGAAGAAGGAAATAATAGTCCTCCCAGAGC 103
                                                                                                                                                                                                                                                                                                                                                                                                                722 ArgalaGlyGlyArgHisValLeuValLeuProAsnAsnSerlleThrLeuAspGlySer 741
                                                                                                                                                                                                                                                              282 CACGTCAGAGGCCCCCAGTGCAGTGGAAAATATTGACAAAGCAATAGCCACTGTG
                                                                                                                                                                                                                                                                                                       ThrGlyLeuGlnValGlyThrTyrHisPheArgLeuThrValLysAspGlnGlnGlyLeu
                                                                                                                                                                                                                                                                                                                      ACTGGTCTCCAGGTGGGGACCTACCACTTCGGTTTGACAGTAAAGACCAGCAGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                102 GGGCTGGTGGCAGACATGTTCTTGTGCTTCCCAATAATTCCATTACTTTGGATGGTTCA
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                                                                                                                                                                                                                                                  HisValArgGlyProSerAlaValGluMetGluAsnIleAspLysAlaIleAlaThrVal
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 284
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403.00
67.57%
62.84%
7.22%
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477.00
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CORGANISM: Homo sapiens
US-10-717-597-68
                                                                  ; ORGANISM: Homo sapiens
US-10-764-390-1
                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-10-764-390-1/c

Sequence 1, Application US/10764390

Publication No. US20040214212A1

GENERAL INFORMATION:
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao

TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: USPERSANCE: 51158-20081.00

CURRENT APPLICATION NUMBER: US/10/764,390

CURRENT FILING DATE: 2004-01-24

PRIOR FILING DATE: 2003-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------TyrGlylleLysHisArgSerThrGluHisAsnSerSerLeuMetVal 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1000 AsnMetAspGlu-----yengluArgMetGluLeuArgProLys 1012
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                                                                    941 IleGlnArgTyrIleTrpAspGlyGluSerAsnCysGluTrpSerIlePheTyrValThr 960
                                                                                                                                                                                                                                                                               938 -----GluAsnLeu 940
                                                                                                                                                                                                                                                                                                                                                                                         961 ValLeuAlaPheThrLeuIleValLeuThrGlyGlyPheThrTrpLeuCysIleCysCys 980
                                                      865 ThrValIleValPheTyrValGlnSerArgProProPheLygValLeuLysAlaAlaGlu 884
                                                                                                             885 ValAlaArgAsnieuHisMetArgieuSeriysGluLysAlaAspPheLeuLeuPheLys 904
                                                                                                                                                                   905 ValLeuArgValAspThrAlaGlyCysLeuLeuLysCysSerGlyHisGlyHisCysAsp 924
 847 ValLeuAspSerAspIleLysValGlnLysIleArg-----AlaHisSerAspLeuSer 864
                 3968 GAT---GAGAATAAGATCCAGGTCAGGAGCTAAAATATGACTTGCATACGGAT---GCT
                                                                                                                            925 ProleuThrLysArgCysIleCysSerHisLeuTrpMet--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1049 GlyAsnProLysValSerMetAsnGlySerIleArgAsnGly 1062
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1014 GlyllelysHisArgSerThrGluHisAsnSerSerLeuMetValSerGluSerGluPhe 1033
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                                                      63 rereacreerreaceaacecrerarerereacecrrrrrreaaregaearrreareaae 122
                                                                                    943 ArgTyr1leTrpAspGlyGluSerAsnCysGluTrpSer1lePheTyrValThrValLeu 962
                                                                                                    300 --- CAGGAAAGCCTGGAGCTGAAGCCAACCTCCCGAGCAGGTAAAGAAAAGAAATGTCA 356
                                                                                                                                                                                                                                                                                                                                                   357 CTGAGTGGCCTGAACCAAAGCTCATGGATACTGGAGATGAAGAACCAGCAGGAGACCCCA 416
                                                                                                                                                                                                                                                                                                                                                                                                           417 gecarcaaacagaaaggccrrrrgcraagragcagccrgargcacrccgagrcagagcrg 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysAspProLeuThrLysArgCysIleCysSerHisLeuTrpMetGluAsnLeuIleGln
3 TTCAGAGCCTTGGAAGTCAACACTGTCACATGTCAGCTGAACTGTTCCGACCATGGCCAC
                                                                                                                                            963 AlaPheThrLeuIleValLeuThrGlyGlyPheThrTrpLeuCysIleCysCysLys
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFRENCE: PS2039P1
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT PILING DATE: 2004-03-12
FRICH APPLICATION NUMBER: US/99/684,524
FRICH APPLICATION NUMBER: PCT/US00/08979
FRICH APPLICATION NUMBER: PCT/US00/08979
FRICH APPLICATION NUMBER: 60/128,693
FRICH APPLICATION NUMBER: 60/128,693
FRICH APPLICATION NUMBER: 60/128,693
FRICH APPLICATION NUMBER: 60/130,991
FRICH FILING DATE: 1999-04-09
FRICH FILING DATE: 1999-04-09
FRICH FILING DATE: 1999-04-09
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Sequence 89, Application US/107:
Publication No. US20040152164A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 89
LENGTH: 1420
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US-10-798-512-89
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Best Local Similarity:
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                                                                                                    LeulleAspGlySerGlnSerThrAspAspThrGlulleValSerTyrHis-----Trp 470
                                                                                                                                                            471 GluGluIleAsnGlyProPheIleGluGluLysThrSerValAspSerProValLeuArg 490
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                                          ProProvalAlavalValSerProGlnLeuGlnGluLeuThrLeuProLeuThrSerAla 452
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               US-10-764-390-3 (1-1072) x US-10-717-597-68 (1-126990)
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Mismatches:
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Matches:
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US-10-050-704-89
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Best Local Similarity:
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US-10-050-704-89
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                                                                                                                                                                                                                                                             243 AGGCAAAAA---GGAAAAACCCAAGAGGAAAAGCAAGTACAAGTCCTGGATGCCACGGAT 299
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                                                        CysAspProLeuThrLysArgCysIleCysSerHisLeuTrpMetGluAsnLeuIleGln 942
                                                                                  63 IGIGACTCGTTCACCAAACGCTGTATCTGTGACCCTTTTTGCATGGAGAATTTCATCAAG 122
                                                                                                                 943 ArgTyrIleTrpAspGlyGluSerAsnCysGluTrpSerIlePheTyrValThrValLeu 962
                                                                                                                                  123 GTGCAGCTGAGGATGGAGAACAGCAACTGTGAGGGGGGGTTATATGTTATATGTTGCT 182
                                                                                                                                                                           963 AlaPheThrLeuIleValLeuThrGlyGlyPheThrTrpLeuCysIleCysCysCysLys 982
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA-034A
CURRENT APPLICATION WEBER: US.10/282,122A
CURRENT PILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                             417 escarcaaacacaaagecerrrrecraagraccaccrearecacrecaagragecre
PhelysValleuArgValAspThrAlaGlyCysLeuLeuLysCysSerGlyHisGlyHis
                1003 GluGlnGluArgMetGluLeuArgProLysTyr----
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Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wandy, Liangeu

APPLICANT: Malone, Cheryl

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Olsen, Kari

APPLICANT: Zyskind, Undith

APPLICANT: Tynkind, Undith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John
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PRIOR FILING DATE: 2000-03-21
PRIOR FLING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR PILING DATE: 2000-05-66
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
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Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-13443
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2010-102-09
PRIOR FILING DATE: 2010-102-09
PRIOR FILING DATE: 2010-102-06
PRIOR FILING DATE: 2010-102-16
PRIOR PLOATION NUMBER: 60/269,308
PRIOR PLING DATE: 2010-102-16
NUMBER OF SEQ ID NOS: 78614
SOUTHARE: Patentin version 3.1
SEQ ID NO 13443
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Burkholderia fungorum
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Best Local Similarity:
Query Match:
DB:
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Sequence 1034, Application US/10278698
| Publication No. US20050037344A1
| GENERAL INPORMATION:
| APPLICANT: PathoArray GmbH
| APPLICANT: PathoMarroy Thomas
| TILLE OF INVENTION: Nucleic Acid Array FILE REFERENCE: 030027US
| CURRENT APPLICATION NUMBER: US/10/278, 698
| CURRENT FILING DATE: 2002-10-23
| NUMBER OF SEQ ID NOS: 1050
| NUMBER OF SEQ ID NOS: 1050
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US-10-278-698-1034
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US-10-278-698-1034
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Sequence 827, Application US/09270767

Sequence 827, Application US/09270767

Patent No. 6703491

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT FILE REFERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0
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Sequence 341, App
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cogn_21/USPTO_spool_p/US10764390/runat 12102005_110204_22353/app_query.fasta_1.1223
-Q=/Cogn_21/USPTO_spool_p/US10764390/runat 12102005_110204_22353/app_query.fasta_1.1223
-DE=ISSUEG PARENES NA -QENT=fastap -SUFPIX=p2n.rni -MINMATCH=0.1 -LGOPCL=0
-LIST=A5 -DOCALIGN=200 -THE SCORE=pct -THE MATE_100 -THE MINE O-ALIGN=15
-MODES=LOCAL -OUTFMY=pto -NORM=ext -HEAPS/IES=500 -MINLENS=0 -MAXIEN=20000000
-USER=US10764390_@CGN 1 1.105 @runat_12102005_110204_22353 -NCPU=6 -ICPU=3
-NO_NMAP -LARERGUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV_TIMEOUT=120 -WARN ITHEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 16109, A
Sequence 484, App
Sequence 2590, Ap
Sequence 6552, Ap
Sequence 3204, Ap
Sequence 3204, Ap
Sequence 39, Appl
Sequence 1013, Ap
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                        ; Search time 414 Seconds (without alignments) 4236.929 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
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1: /cgn2_6/ptOdata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptOdata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptOdata/1/ina/5B_COMB.seq:*
4: /cgn2_6/ptOdata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptOdata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptOdata/1/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                          nucleic search, using frame_plus_p2n model
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US-09-270-767-16109
US-09-902-540-484
US-09-902-540-1119
US-09-902-540-1119
US-09-248-76552
US-09-248-76540-3204
US-09-902-540-2872
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Sequence 484, Application US/09902540

; Sequence 484, Application US/09902540
; Patent No. 683447
; GENERAL INFORMATION:
; APPLICANT: Gladman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Wiegand, Roger C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTYON: WAXOCOCCUS xanthus Genome Sequences and Uses Thereof;
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR PRILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 484
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613 ValThrValIleValGlnProGluAsnAsnArgProProValAlaValAlaGlyProAsp 632
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                                                    SerSerAspAspHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySerGluGly
                                                                                                                LysHisValValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMetGlnGlu
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ORGANISM: Myxococcus xanthus
US-09-902-540-484
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US-09-270-767-16109/c

iSequence 16109, Application US/09270767

iSequence 16109, Application US/09270767

iSequence 16109, Application US/09270767

iSequence 16109, Application US/09270767

iGENERAL INFORMATION: Nucleic acids and proteins of Drosophila melanogaster

iTILE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

iTILE OF INVENTION: NUMBER: US/09/270, 767

iCURRENT FILING DATE: 1999-03-17

iNUMBER OF SEQ ID NOS: 62517

iSEQ ID NO 16109

iSEQ ID NO 16109

iTYPE: DNA

TYPE: DNA

TYPE: DNA
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      AsnSerThrThrAlaAlaLeuIleValAsnAsnAlaValAspTyrProProValAlaAsn
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TGTGG-GCCTCCATGCTCTGG	1856 AAGGTGAATGAGACCGGCGCCTTCTCGTTCAGCTTCCGCTACCGC 1900 286 rValGluLysSerProValLeuThrValThrProGlySerThrGluHisSerIleProTh 306 286 rValGluLysSerProValLeuThrValThrProGlySerThrGluHisSerIleProTh 306 1901 CACTCGTTCGAGTCCGACATCTACCCGGCGGCT
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GATGTACCGCAACGC----- 2100 CGGGTGGACGAGCAGGCGACGGCGCCA 2336 :::|||| cgcgacgrcgcagccccagcgccccgg 2396 ||||||| |GCACTGGAGCTCGTGCGCCACACGCTGG 2456 ::::::|||||||||| cccctcacctaccactggacgcaggtga 2516 |||| |GTGCCCGACGACTCCATCCTGACGTTCC 2603 Acecceaecrrcaaecrecceaegree 2870 GTGAACCACTGCAGGGACCAGGA 2930 CGGCAAGACGGTGCGCTTCCCGGAGTGG 2158 TACGGCTTCGACCTGGACGTGCGCT 2276 IlevalSerTyrHisTrpGluGluIleA 474 ThrProTyrLeuHisLeuSerAlaMetG 591 AsnAsnArgProProValAlaValAlaG 630 GluThrThrTyrAsnTyrGluTrpAsnL 374 IleLysGlnGly----- 388 ServalGlyLeuTyrVal---PheLysV 407 -----GlyP 419 -----SerProG 441 AlaLeu-----IleA 455 AspSerProValLeuArgleuSerAsnL 494 ValThrAspSer----- 508 Thr -----Thr Ala Ala Leuilev 521 AsnAlaGlyProAsnHisThrIleThrL 541 TrpSerLeuGlyProGlySerGluGlyL 573 ValThrAspSerSerArgGlnGlnSerT 610 leThrLeuProAspAsnGluValGluLe 354

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Sequence 2590, Application US/09902540

Ratent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION WUMBER: US/09/902,540

CURRENT APPLICATION WUMBER: 00/217,883

FILM APPLICATION NUMBER: 60/217,883

FRIOR APPLICATION NUMBER: 60/217,883

FRIOR FILING DATE: 2000-07-10

FRIOR FILING DATE: 2000-07-10

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              lyProAspLysGluLeuIlePheProValGluSerAlaThrLeuAspGlySerSerSerS
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                                                                                           GluMetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeuGlnVal-----
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Mismatches:
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317.00
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184 AspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsnSerSerValGlyAspSerPro 203

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2707 GTGTTCACGCTGACCGTCTCCGACGGCGTCAAGACGTCCACGGACTCGGTGACCGGTGACG 2766
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2767 GTGGCGCTCCCCAACAATCCGCCCACCGTGAACGCGGGCCTCGACGGCATCGTCGAGGAG
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                                                                    AlaGluThrGlnGlnAspProGluLeuHisTyrLeu
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Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Mysococcus xanthus Genome Sequences and Uses Thereof;
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT PILICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825
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3454 ATCGGTGC-----ACGGATGTGACCCTGACGGCGCCGACACCCTGACGCCGTCG 3504
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                                         TrpSer---LeuGlyProGlySerGluGlyLysHisValValMetGlnGlyValGln---
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                                                                            SerAspGlyAlaThrAsnSerThrThrAlaAlaLeuIleVal------AsnAsn
                                                                                                       3565 GGCACCTCGACCACCACGGATGCCGTGCGCGTCATCGTGGCGGCGGGGCGGACCCGGGTGCCAAC
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US-09-902-540-1119
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LENGTH: 16584
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; ORGANISM: Myxococcus xanthus
US-09-902-540-1119
                                                                                                                             Percent Similarity:
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Query Match:
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US-09-902-540-6552 ; Sequence 6552, Application US/09902540 ; Patent No. 683347 ; GENERAL INFORMATION:

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    --ProAsnLeuGluThrThrArg

APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
APPLICANT: Misgand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses ?
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6552
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Mismatches:
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ence 3204, Application US/09248796A
ent No. 674137
ERAL INFORMATION:
ERAL INFORMATION:
ERAL INFORMATION:
ILE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN-
ILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
LE REFERENCE: 107196.132
RRENT APPLICATION NUMBER: US/09/248,796A
RRENT FILING DATE: 1999-02-12
IOR APPLICATION NUMBER: US 60/074,725
                                     2543 CGGACACGCCACCCCGTCGTTCACGGCGGATGTGCCCGACGACTCCATCCTGACGTTCC 2602
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spGlySerGlnSerThrAsp---AspThrGluIleValSerTyrHisTrpGluGluIleA 474
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 3204
LENGTH: 2481
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215.50
32.80%
22.47%
3.86%
                                                                                             TYPE: DNA ORGANISM: Candida albicans
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Best Local Similarity:
Query Match:
DB:
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US-09-248-796A-3204
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Pred. No.:
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Batent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Gldman, Roger C.

APPLICANT: Slater, Steven C.

APPLICANT: Blater, Steven C.

APPLICANT: Blater, Steven C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT APPLICATION NUMBER: 60/217,883

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 2872

LENGTH: 1119

TYPE: DNA
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1941 TTCTGGATCTGAACCAGTATTGATACCAATACAGTT--------GCTTC 1982
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2322 AGTTACTGGTAGTGAATGAATTTTGACTGGTAATACTGAAAGAAGTGCTACTGCTATTGC 2381
1731 TGATACTACTGCTGGCGCTAGTTCAACTGCCAGTGAAGCAACTGCT-----GAGAATTT 1784
                                               ------- CA 1823
                                                                 uAspGlySerSerSerAspAspHisGlyIleValPheTyrHisTrpGluHisValAr 664
                      594 pTyrThrPheGlnLeuLyBValThrAspSerSerArgGlnGlnSerThrAla ***ValTh 614
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                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                          2.34e-09
207.50
41.40%
25.54%
3.72%
; ORGANISM: Myxococcus xanthus US-09-902-540-2872
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Best Local Similarity:
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                                                                       ---CTGCCGCG 9777
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                                                                                                                                           697 AspGlnGlnGlyLeuSerSerThrSerThrLeuThrValAlaValLys-----Ly
                                                   TyrProProValAlaAsnAlaGlyProAsnHisThrIleThrLeuProGlnAsnSerIle
                                                                                                                       547 ThrieuAsnGlyAsn---GlnSerSerAspAspHisGlnIleValLeuTyrGluTrpSer
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COUNTRY: US
ZIP: 53701-2113
COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
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TITLE OF INVENTION: No. 6365723el Sequences of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
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STREET: 1 South Pinckney Street
CITY: Madison
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Plunkett, Guy
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   ThrvalThrGlyLeuGlnValGlyThr -----TyrHisPheArgLeuThrValLys 696
                           CAGTICACCGCGCCTGAGGTCTCAGCCGCAACGGAGTTCGTCTTCGTGGTGAAGGTCTCC 954
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof FILE REFREENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PILLING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1013
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1015 GCGCCGAAGGAGTCCAGCGGTTGCTCGTCCACCGGGACGA-
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Indels:
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Sequence 1013, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
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Best Local Similarity:
Query Match:
DB:
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5745 GTTGATCTCACCGCCGTCGCCATCAGCATGAACAGCATCACCAGCGATGATGCGATTAAC 15804
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                                                363 ProvalGluThrThrTyrAsnTyrGlu---TrpAsnLeulleSerHisProThrAspTyr
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157
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283
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                                                          FILING DATE: 03-Dec-1999
CLASSIFICATION: 4Unknown>
PRIOR APPLICATION: 4Unknown>
PRIOR APPLICATION DATE: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-764-390-3 (1-1072) x US-09-453-702B-39 (1-25165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                APPLICATION NUMBER: US/09/453,702B
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORD PERFECT 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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34.40%
20.85%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                         NAME/KEY: misc feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a,
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ON: (98266)..(98266)
INFORMATION: n equals a,
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ION: (148948)..(148948)
INFORMATION: n equals a,
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ION: (191589)..(191989)
INFORMATION: n equals a,
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TION: (224187)...(234187)
R INFORMATION: n equals a,
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THER INFORMATION: n equals a,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (622708)...(622708)
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INFORMATION: n equals a,
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CON: (103998) .(103998)
INFORMATION: n equals a,
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ION: (163385)..(163385)
I INFORMATION: n equals a,
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ION: (191995)...(191995)
! INFORMATION: n equals a,
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LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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INFORMATION: n equals a,
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a,
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CON: (559167)..(559167)
INFORMATION: n equals a,
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INFORMATION: n equals a,
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                                                                   NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
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FION: (98239)..(98239)
RINFORMATION: n equals
                                        ION: (84812)..(84812)
INFORMATION: n equals
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APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
Patent NO. 6503729
TITLE OF INVENTION: jannaschii
FILE REFRENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16849 GATGTTGCGGCACTCAGTGATGGCACCAGCTTACGGTTAGCGCCTCCGCTCAGGACAGT 16908
                                             16624 CAGACGCACAACGTACAGGTGAACACGGCGGCAGTGTCGCTCTCGGTCAGCACTATCAGC 16683
                                                                                                                                                                                                                                                                              16789 AAAGGCTACAGCGCCACCATTCAGAGCAACGGGAGCTGGAGCGTGAACGTGCCTGCGGCG 16848
16384 GGCGATGATGTGATTAACAACGTCGAACACTTCAGGCGCAGATTATCAGCGGCACCGCC 16443
                                                                                                                                                                                                                                                                                                                                                                    769
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                                                                                                                                                                                                                                                      714 GluAsnAsnSerProProArgAlaArgAlaGlyGlyArgHisValLeuValLeuProAsn 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                778 ---LeuThrAsnieuValGluGlyVal---TyrThrPheHisLeuArgValThrAspSer 795
                           645 AspGlySerSerSerSerAspAspHisGlyIleValPheTyrHisTrpGluHisValArg 664
                                                                                                                                                                                             665 GlyProSerAlaValGluMetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeu
                                                                                                                                      685 GlnValGlyThrTyrHisPheArgLeuThrValLysAspGlnGlnGlyLeuSerThr
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COCATION: (84773)
OTHER INFORMATION: n equals a, t,
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LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a,
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LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a,
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SOFTWARE: Patentin version 3.1
FRO ID NO 1
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US-08-916-421B-1/c
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ORMATION:	(657081)(NAME/KEI: MISC FEATURE LOCATION: (657203)(657203) OTHER INFORMATION: n equals a,	misc_featur (674435)(DRMATION: n	KEY: misc feature ION: (682442)(682442) INFORMATION: n emale	KEY: misc feature ION: (713652). (713652) INSTORMATION: n ornale	KEY: misc feature ION: (741684)(741684)	KEY: misc feature ION: (779455)(77945 INFORMATION: n equal	KEY: misc_feature_ ION: (779676)(7796 INFORMATION: n equa	KEY: misc featur ION: (855539)(INFORMATION: n	KEY: misc featur ION: (871619)(INFORMATION: n	: misc_featur : (1084830) FORMATION: n	: m18C : (1096 FORMATI	misc featur (1119881) ORMATION: n	misc featur (1130881) ORMATION: n	misc fea (1310988 DRMATION:	NAME/KEY: misc feature LOCATION: (1313224)(1313224) OTHER INFORMATION: n equals a,	misc fe (134 <u>9</u> 47 DRMATION	: misc_featur : (1349491) FORMATION: n	: misc_featur : (1470091) FORMATION: n	: misc_featur : (156 <u>9</u> 020) FORMATION: n	misc featur (1602912) RMATION: n	YEY: misc featur FION: (1603734)	YEY: misc fea FION: (1637998 INFORMATION:	NAME/KBY: misc_feature LOCATION: (1664854)(1664855) OTHER INFORMATION: n equals a,

US-08-9	916-4211	B-1				
Alignment Pred. No. Score: Percent S Best Loca Query Mat	it Scini Simi Sal S	ores: larity: imilarity:	0.00462 35.63\$ 22.57\$ 3.60\$	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1664976 128 217 149 26	
US-10-7	64-390	-3 (1-1072	2) x US-08-916-4	421B-1 (1-1664976	•	
상 염	298 33829	GlyserThrGl ::: GGAATATAGA	uHisSerIl GGTTGGAAT	답 :	rProProThrSerAlaAlaProSerGluSerThr -CCACCAATTGGAGGTTGGAGGATACAGCAGTTAT	317
È	318	ProSerGlu	ProSerGluLeuProlleSerPro	roArg 	erProThrThrAlaProArgThrValLysGluLeuThrVal	337
ąg	33772	ccrca	– ⊱	- -5	ACTTACTATCCAATAAATATA	33719
රු සි	338	SeralaGly	aGlyAspAsnLeuIleIleThrLeuProAspA	ThrLeuProAspAsnG	snGluValGluLeuLysAlaPhe	357
ે ક	358	ValAlaProAla	ProP	roValGluThrThrTyrAsnTyrGluT ::::::::::::::::::::::::::::::::::::	ThrTyrAsnTyrGluTrpAsnLeulleSerHis	377
}	37	ProThrAsp	ProThrAspTyrGlnGlyGlu	kieli	ysGlnGlyHisLysGln	391
đ	33673		 TATTTCGGAGATGG	 rgccagtctttggataa		33623
È	39	ThrLeuAsi	ThrLeuAsnLeuSerGlnLeuSer	erValGlyLeuTyrValP	ThrieuAsnieuSerGlnLeuSerValGlyLeuTyrValPheLysValThrValSerSer	Ħ
셤	N	ACTTTCAC	ACATACATACACTTC	AGAAGGGGTTTATCCAA	TATATATGAAAGTTTATACT	0
දු ද	412	GluAsnAle GCAGAAAA1	aPheGlyGluGlyPhe ::: TATGAAACAGTATAT	eValAsnValThrValL GTAATAGACAATAAAA	GluAsnAlaPheGlyGluGlyPheValAsnValThrValLysProAlaArgArgYalAsn 	431 33503
ŏ	432	a	aValVa	rPro-GlnLeuGlnGlu	nLeuGlnGluLeuThrLeuProLeu	449
q	33502	ATTTATCCA		: :: rcctgcaagttataaag	:::	33455
ò	450		ThrSerAlaLe	SerAlaLeulleAspGlySerGlnS	SerThrAspAspThrGlu	464
Dp	33454	ATAAATAGI	rtatgacccagatgc:	I I I I I I I I I I I I I I I I I I I	ATAAATAGTTATGACCCAGATGCTAATAGAATGATTCCAGAGTATAATTACTACGGCACC	33395
Š	465		[1	<pre>IleValSerTyrHisTrpGluGl :::</pre>	GluGlu	472
qq	33394	TTAATAGGC	STATTATCCTATATC	rccaactcacccarde	TTAATAGGGTATTATCCTATATCTCCCAAACTCACCCATGGCAAGAATATATGGGTTTTAAC	33335
& 8	473	TTAACAGT		IleAsnGlyPro :::::: AAATGTTGCATGGAAT-		483
Š	483	rvalAspSe	rProValLeuArgLe	euSerAsnLeuAspPro	rValAspserProValLeuArgLeuSerAsnLeuAspProGlyAsnTyrSerPheArgLe	503
q	33275	TATTATATCC		::: AAAAGTTTTCCTATA	::: AAAAGTTTTCCTATAGGGAATTACACTGCTAAATT	33231
Ğ	503	uThrValTh	uThrValThrAspSerAspGlyAlaThrAsnS	aThrAsnSerThrThr	rThrAlaAlaLeuIleValAsnAs	523
Db	33230		3GGATGGAATGGGAGG	GGTAGTTTGGGATGGAATGGGAGGAGTTAATTCAACAACTGTTAAGTTTAGTGTG	GTTAAGTTTAGTGTG	33176
양. 원	523 7 33175	nAlaValA£ :::: ATAA	spryrProProvalal :: \	nalavalaeptyrbroprovalala	AsnAlaGlyProAs CCAGATAAACCTGAACCTAA	536 33120
ઠે	536		leThrteuProGlnAs	nHisThrIleThrLeuProGlnAsnSerIleThrLeuAsnGlyAsnGlnS	GlyAsnGlnSerSerAspAs	556
qq	33119		ragaattcgtttccc	TGAGGATGTAGAATTCGTTTTCCCAGTCTTATGACCCGGAGGG	.dgT	33077
ኞ.	. 556		leValLeuTyrGluT)	pHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySerGluGlyLysHi	SerGluGlyLysHisValVa	576

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LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t,
FBATURE:
                                                       ORGANISM: Methanococcus jannaschii
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ION: (84773)..(84773)
INFORMATION: n equals a,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a,
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OCATION: (98343)..(98343)
VTHER INFORMATION: n equals a,
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals
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LOCATION: (84808)..(84808)
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
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LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals
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ION: (98266)..(98266)
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APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: jannaschii
FILE REFERENCE: PAPAGE
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/916,421
PRIOR APPLICATION NUMBER: US 60/916,421
PRIOR FILING DATE: 1996-08-22
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33035 TATCAATACAACAGATACG---ATAGTTCATCACAAATATGAAAGACCAGGCTACTATAC 32979
                                                                                                                                                              32978 AGTTACCTTAACAGTATTTGACAATATAACGCAAGTAGTTCCAATATCAAAACAAATAGT 32919
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                                                                                                                                                                                                                                                                   670 uMetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeuGlnValGlyThrTyrHi 690
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                                                                                                                           596 rPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThrAla***ValThrValIl 616
                                                                                                                                                                                             616 eValGlnProGluAsnAsnArgProProValAlaValAlaGlyProAspLysGluLeuIl
                                                   576 iMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAspTyrTh
                                                                                                                                                                                                                                                                                                      32879 AAATGAAAATACTGTAAGATTTGAAGATACATCAGTTGTGGCCCCTGGGGAA------
                                                                                                                                                                                                                                                                                                                                         650 rAspAspHisGlyIleValPheTyrHisTrpGluHisValArgGlyProSerAlaValGl
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NAME/KEY: misc feature LOCATION: (234220)(234220) OTHER INFORMATION: n equals	FEATURE: NAME/KER: LOCATION: (234814)(234814) OTHER INFORMATION: n equals	FEATURE: NAME/KEY: misc feature LOCATION: (309398)(309398) OTHER INFORMATION: n equals	FEATURE: NAME/KEY: misc feature LOCATION: (309418)(309418) OTHER INFORMATION: n equals	NAME/KEY: misc feature LOCATION: (312837)(312837) OTHER INFORMATION: n equals	FEATURE: NAME/KEY: misc feature LOCATION: (312993). (312993) OTHER INFORMATION: n equals a	NAME VOE: NAME VOE:	FALUNE: NAME/KEY: misc feature LOCATION: (559167)(559167) OTHER INFORMATION: n equals	NAME/KEY: misc feature LOCATION: (559241)(559241) OTHER INFORMATION: n equals	FEATURE: MAME/KEY: misc_feature LOCATION: (600992). OTHER INFORMATION: n equals	FEATURE: FARTURE: LOCATION: (622708)(622708) OTHER INFORMATION: n equals	FEATURE: MARKES: LOCATION: (657081)(657081) OTHER INFORMATION: n equals	FEATURE: NAME/KEY: misc feature LOCATION: (657203) (657203) OTHER INFORMATION: n equals	FEAUNE: NAME/KEY: misc feature LOCATION: (674435)(674435) OTHER INFORMATION: n equals	FAGUNE: NAME/KEY: misc feature LOCATION: (682442)(682442) OTHER: INFORMATION: n equals	NAME/VES: misc feature LOCATION: (713652) (713652) OTHER INFORMATION: n equals	misc feature (741684)(741684 DRMATION: n equals	FEATURE: NAME/KEY: misc_feature LOCATION: (779455)(779455) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc_feature

33712 GTAGAGCCGGCA------33674 33718 ACA-----ATA 33713 298 GlySerThrGluHisSerIleProThrProProThrSerAlaAlaProSerGluSerThr 317 318 ProSerGluLeuProlleSerProThrThrAlaProArgThrValLysGluLeuThrVal 337 338 SerAlaGlyAspAsnLeuIleIleThrLeuProAspAsnGluValGluLeuLysAlaPhe 357 358 ValAlaproAlaProProValGluThrThrTyrAsnTyrGluTrpAsnLeuIleSerHis 377 378 ProThrAspTyrGlnGlyGlu------ileLys---GlnGlyHisLysGln 391 392 ThrLeuAsnLeuSerClnLeuSerValGlyLeuTyrValPheLysValThrValSerSer 411 Length:
Matches:
Conservative:
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Indels: US-10-764-390-3 (1-1072) x US-09-692-570-1 (1-1664976) ρ þ b c, or g ö ö ö ö or or ö ö ů ΰ ΰ ϋ NAME/KEY: misc feature LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals a, t, ŭ FEATURE:
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t,
FRATURE:
NAME/KEY: misc feature
LOCATION: (871619)..(871619) PEATURE:
NAME/KEY: misc_feature
LOCATION: (1084830)
OTHER INFORMATION: n equals a, FEATURE: NAME/KEY: misc_feature LOCATION: (1096846)..(1096846) OTHER INFORMATION: n equals a, FEATURE:
NAME/KEY: misc_feature
NOCYTION: (1119881)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1349473)..(1349473) OTHER INFORMATION: n equals a, 0.00462 201.00 35.63% 22.57% 3.60% LOCATION: (779676)..(779676) OTHER INFORMATION: n equals Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.: δ g ò g ઠે ద ઠે 요 ò 셤 ò

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APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Mysococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
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APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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APPLICANT: Hinkle,
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Best Local Similarity:
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Mismatches:
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Matches:
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1136
; LENGTH: 16047
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1136
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APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Services
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13278 cccacertritacicaccaararrancececececerarcicaccericacera 13337
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 99352
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-764-390-3 (1-1072) x US-08-853-659A-5 (1-15512)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Processor (WordPerfect 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      Paul W. Zimmerman
Intellectual Property Servic
Battelle Memorial Institute
PNNL P.O. Box 999
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STRANDEDNESS: double stranded
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20.60%
3.51%
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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STREET: Washington Way
CITY: Richland
STATE: Washington
COUNTRY: U.S.A.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15512 bases
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Best Local Similarity:
                               GENERAL INFORMATION:
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| B58 CACGCGGAACCAGCCGTAGGCTACTTCTTGTGCTGCATCGCCGAGGCGATCAGGT 4801
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                                                      oValAlaAsnAlaGlyProAsnHisThrIleThrLeuProGlnAsnSerIleThrLeuAs
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5701 CGGCGCCATCGCCAGCGAGGAAGCCGTGGTCATGGTGGAC---
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à	683 GlyLeu	GlyLeuGlnVal	686
qo	14541 GGAACG	 GGAACGACAACCTCGTTTACTGCGACACAGGGGCTGGAGGATGGAGCTTTACACCGCCA :	14600
à	687		701
qq	14601 GCGCCG	SATCGGGGGGGAAAT	14660
ć	702 SerSer	SerSerThrSerThrLeuThrValAlaValLysLysGlu	714
qa	14661 ACGCGT	ACGCGTCCGTCTACCCCGCTGACGGTGACAGTGGGATACGCAATAGCCATTGATCGTATT	14720
ò	715	erProProArgAlaArgAlaGlyGlyArgHisVal	728
q	14721 GAATTA	GAATTAGTCAACGATAGCGGCGTCCCTGGCGATAATGTGACAAAACATGTGCGTCCGCAG :	14780
ò	729		742
qq	14781 TTCCAG	TTCCAGATCTCGGTACCGGATGATGT-GGAAAAGTTCTTCTGAGTATTGACGGCGCACG	14839
ò	743 SerThr	ArgAspGlyGlnSerProAla	762
qq	14840 ACC		14869
۶,	763 Alagly	pHisSerValAlaLeuGlnLeuThrAsnLeuVal	782
QQ	14870 GCTGGC		14908
ò	783 GluGly	3]uGlyValTyrThrPheHisLeuArgValThrAspSerGlnGlyAlaSerAspThrAsp	802
QQ	14909 GAGGGA	GAGGGACAGCATACCCTGACCGTGGAAGTGACTGACGCTGCGGGTAATAAGATGACGGAG	14968
δχ	803 ThrAla	ThralaThrvalGluvalGlnProAspProArgLysSerGlybeuValGluLeu	820
qa	14969 ACGCTC	ACGCTCAATTTCACTATCGATATCACGTTGTTAACGCCA	15007
ò	821 ThrLeu		837
qq	15008 ACCATT		15067
ò	838 ValArg	ValArgGInLeuAlaValLeuLeuAsnValLeuAspSerAspIleLysValGInLysIle	857
Д	15068 GTCACT	À	15115
λΌ	858 ArgAla	ArgAlaHisSerAspLeuSerThrValIleValPheTyrValGlnSerArgProProPhe	877
DÞ	15116		15151
ογ	878 Lygval	LysValLeuLysAlaAlaGluValAlaArgAsnLeuHisMetArgLeuSerLysGluLys	897
qa	15152 AAAACG	::: AAAACGGTGGTACTCACCGAATCAGCCGACGGCTGGCGCTATCGACCGGATTCTGCTTTG	15211
λ	898 AlaAsp	AlaaspPheLeuLeuPheLysValLeuArgValAspThrAlaGly 912	
qa	15212 GCGGAC	degeacgetagctacattcaccgtgacggtaacagatgtggcaggc 15259	

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Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130043K22 product:hypothetical PKD domain containing protein, full insert sequence.
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CR566736
CB519102
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BQ267742
BD267742
BM547013
CB527694
BQ768962
BM479855
AL589494
BE311921
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AU132238
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CN365571
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CF170107
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AK051381.1 GI:26094501
HTC; CAP trapper.
Mus musculus
226.4
118.8
117.9
117.9
116.3
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RESULT 1
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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 Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2 1/05F00 spool pV4S10764390/runat 12102005 110203 22340/app_guery.fasta_1.1223
-Q=/cgn2 1/05F00 spool pV5107F1x=p2n.rst -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LifsT=45
-DOCALIGN=200 -THR SCORE=pct -THR_MAX=100 -THR MIN=0 -ALIGN=15 -MODE-LOCAL
-UOTFWHEPAD- -NORME=xt -HEAPSIZE=560 -MINIENS=0 -MAXENS=2000000000
-USER=US10764390 @CGN 1 1 5.180 @runat 12102005 110203 22340 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AK043006 Mus muscu
AR031342 Mus muscu
AL834315 Homo sapi
AY417695 Mus muscu
AY417693 Homo sapi
AY417694 Pan trogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscu
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                                                                                                     ; Search time 6860 Seconds (without alignments) 5948.236 Million cell updates/sec
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                                                                                                                                                                                             MAPPIGVLSSLLLLVTIAGC......VSMNGSIRNGASFSYCSKDR 1072
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                          nucleic search, using frame plus p2n model
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                                                                                                                                                                                                                                                                                                                                                  of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AK084668
AK043006
AF289597
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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9b htc: *
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9b est4: *
9b est6: *
9b est6: *
9b est6: *
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Radachi,J., Alzawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hiramoko,K., Hiramoka,T., Hirozane,T., Hayafata,M., Hayafata,J., Kojima,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kaya,S., Kurihara,C., Matsuyama,T., Miyazaki,M., Murata,M., Nakamura,M., Nomita,K., Nomura,K., Nomura,K., Ohno,M., Ohasto,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Saeaki,D., Shibata,K., Shinagawa,A., Takahashi,T., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. Toya,T., Yasunishi,A., Direct Submission Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, I-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.jp, URL:http://genome.gec.riken.jp/, Tel:81-45-503-9216, Pax:81-45-503-9216, Colone Exploration Research Group Ryploration Research Group Exploration Research Group Exploration Research Group Exploration Research Group Division of Experimental Animal Research in Riken contributed to Division of Experimental Animal Research in Riken contributed to
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/mol_type="mRNA"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PaNTOM_DB:D130043K22"
/db_xref="PaNTOM_DB:D130043K22"
/db_xref="taxon:10090"
/c1one="D130043K22"
/tiseuc_type="spinal ganglion"
/clone_lib="spinal ganglion"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="l2 days embryo"
/dev_stage="l2 days embryo"
/note="hypothetical PKD domain containing protein
/InterPro|IPR000601, evidence: InterPro)
putative"
                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 4828)
                                                                                                                                                   The RIKEN Genome Exploration Research Group Phase II Team and the
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                    a full-length mouse cDNA collection
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Please visit our web site for further details.
URL:http://ganome.gc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Conservative:
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                                                                                                                                                                   FANTOM Consortium.
Functional annotation of a
Nature 409, 685-690 (2001)
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MetalaProProThrGlyValLeuSerSerLeuLeuLeuLeuValThrIleAlaGlyCys 20
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                                                   ACTITICETGCGCAGACCTGTCCAGAGGCCCGGGCAGCTGCTGGACTATGGAGACATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GluLeuHisTyrLeuAsnGluSerAlaSerThrProAlaProLysLeuProGlu
                                                                                                                                                                                          21 AlaArgLysGlnCysSerGluGlyArgThrTyrSerAsnAlaValileSerProAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                               GluThrThrArgIleMetArgValSerHisThrPheProValValAspCysThrAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 GAAACCATCAGAATCATGCGGGTGTCTCAAACCTTCTCCGTGGGAGACTGCACGGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuVal
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	2475 CTTCCCAATAATTCCATTACTTGGATGGTTCAAGGTCTACTGATGACGAGGAAGAATTGTG 2534 751 SerTyrLeuTrpIleArgAspG1yG1nSerProAlaAlaG1yAspVal11eAspG1ySer 770	771 AspHisSerValAlaLeuGlnLeuThrAsnLeuValGluGlyValTyrThrPheHisLeu 790 2578	ALGVALLIITABDOBLGLINGLYALASGLABDIIIILABDIIILABDIIILABDIIILABDIIILABDIIILABDIIILABDIIILABDIIILABDIIIILABDIIILABDIIILABDIIILABDIIILABDIIILABDIIILABDIIILABDIIILABDIIIILABDII	ABPLTOARGU/BSETGLYLEUVALGLULLEULINFELGLINALGLYVALGLYVALGLINE :::	Gludinargiyysaspinirlenvalargdinienalavallenienasnyalienaspiser :::	H-H	ValGInserargProproPheLysValieuLysAlaAlaGluValAlaArgAsnieuHis 	MetargleussriyaGluiyaAlaAspPheiseuseubheiyaValleuArgValAspThr 	911 AlaGlyCysLeuLeuLysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCys 930 	IleCysSerHisLeuTrpMetGluAsnLeuIleGlnArgfyrIleTrpAspGlyGluSer 	951 AbnCysGluTrpSerIlePheTy?ValThrValLeuAlaPheThrLeuIleValLeuThr 970 	GlyGlyPheThrTrpLeuCysIleCysCysCysCysLyshrgGlnLysArgThrLysIleArg	D(5	ProLysTyrGly11e1y8HisArgSeTThrGluHisAsnSeTSeTLeuMetValSerGlu 		1051 ProlygValSerMetAsnGlySerIleArgAsnGlyAlaSerPheSerTyrCysSerLys 1070	1071 Asparg 1072
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351 GluValGluLeuLysAlaPheValAlaProAlaProProValGluThrThrTyrAsnTyr 370	::: :::	Secondicione de la completa del completa de la completa del completa de la completa del completa del completa de la completa del completa d	431 AsnLeuProProValAlaValValSerProGlnLeuGlnGluLeuThrLeuProLeuThr 450	451 SeralaLeulleAspGlySerGlnSerThrAspAspThrGlulleValSerTyrHisTrp 470 	471 GluGluIleAsnGlyProPheIleGluGluLysThrSerValAspSerProValLeuArg 490 ::::: :::	491 LeuSerAsnLeuAspProGlyAsnTyrSerPheArgLeuThrValThrAspSerAspGly 510 	511 AlaThrAsnSerThrThrAlaAlaLeuIleValAsnAsnAlaValAspTyrProProVal 530 	531 AlaAenAlaGlyProAenHieThrIleThrLeuProGlnAenSerIleThrLeuAenGly 550 	551 AsnGlnSerSerAspAspHisGln1leValLeuTyrGluTrpSerLeuGlyProGlyser 570	GluGlyLysHisValValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMet 	591 GlnGluGlyAspTyrThrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThr 610 	Ala***valThrvalIlevalGlnProGluAsnArgArgProProValAlaValAlaGly	erser GCAGT	AspasphisGlyIleValPheTyrHisTrpGluHisValargGlyProSerAlaValGlu 	671 MetGludsnIleAspLysAlaIleAlaThrValThrGlyLeuGlnValGlyThrTyrHis 690 	1 PheArgleuThrVallysAspGlnGlnGlyLeuSerSerThrSerThrLeuThrValAla	zaso ilcogolinacceledenencenecaegelcionecaegelcaccelcaccelegel 211. 711 ValLysElysGluAsnAsnSerProProArgAlaArgAlaGlyGlyArgHisValLeuVal 730

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VSQLTERLKGMLIRQIGVLLGSVLDSDIIVQKIQPYTEGSTGML
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KVOLBADGSWOCEWSVLYVI IASFVIVVALGIISMTTICOCKROKOKRYKKSKRILDA
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/translation="MEKGLGVKPSPASWVLPGYCWQTSVKLPRSLYLLYSFFCFSVLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 ACACITIAIGGAGCIGGCIIGAGAACIGAGGGAGAA---AAICACCICCGGCIICIIGCA 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="13 days embryo"
100. _1357
100. _1357
Note="unnamed protein product; HYPOTHETICAL 103.9 KDA
PROTEIN homolog [Homo sapiens] (SPTR|AAL55781, evidence:
FASTY, 85.5%ID, 97.4%length, match=2763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 AlaTrpTrpPheGluGlyArgCysTyrLeuValSerCysProHisLysGluAsnCysGlu 89
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524
138
295
109
                                                                                                                                                                          prepare mouse tissues.
Please visit our web site for further details.
URL:http://ganome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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Best Local Similari
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Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330027H07 product:HYPOTHETICAL 103.9 KDA PROTEIN MONOLOG [Homo sapiens], full insert sequence.
                                                                                                                                            HTC 03-APR-2004
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 3660)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Submitted (16-JUJ-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
WRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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Analysis of the mouse transcriptome based on functional annotation
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Please visit our web site for further details.
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PROTEIN homolog [Homo sapiens], full insert sequence.
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Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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EVAAMLKSELÖKQKDPELI REPUTCQLNCSDHƏHCDSFTKRCYCDPFWNENFI
KVQLRDGDSNCEWSVLYVI IASFVI VVALGILESWTTI CCCKRQKGKPKRKSRYKILDA
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                       205. .3462
/note="unnamed protein product; HYPOTHETICAL 103.9 KDA
PROTEIN homelog [Home sapiens] (SPTR[AAL55781, evidence:
FASTY, 85.5%ID, 97.4%length, match=2763)
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                      eValLeuThrGlyGlyPheThrTrpLeuCyBileCyBCySCySLyBArgGlnLyBArgTh 987
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Qin, W.X., Zhou, X.W., Zhang, P.P., Jiang, H.Q., Huang, Y., Zhao, X.T.
Wan, D.F. and Gu, J.R.
Novel human cDNA clones with function of inhibiting cancer cell
                                                    gAsnLeuHisMetArgLeuSerLysGluLysAlaAspPheLeuLeuPheLysValLeuAr
                                                                                                                   2844 AATCAGCACAGTCACATGTCAGCTGAACTGTTCTGACCATGGCCACTGTGACTCATTCAC
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Qin,W.X., Zhou,X.M., Zhang,P.P., Jiang,H.Q., Huang,Y., Zhaman,D.F. and Gu,J.R.
Direct Submission
Submitted (17-UTL-2000) National Laboratory For Oncogenes Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, 200032, P. R. China
Location/Qualifiers
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Homo sapiens clone pp791 unknown mRNA.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="pp791"
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Mus musculus 13 days embryo male testis cDNa, RIKEN full-length enriched library, clone:6030408013 product:HYPOTHETICAL 103.9 KDA PROTEIN homolog [Homo sapiens], full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3067)
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Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
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                                                                                                  1028 ValSarGluserGluPheAspSerAspGlnAspThr1lePheSerArgGluLysMetGlu
                                                                                                                                                                                                                                      2827 CACTCCGAGTCAGAGCTGGACAGCGAC--GATGCCATCTTTACATGGCCAGACCGAGAG
                 ThrolyglyPheThrTrpLeuCysIleCysCysCysLysArgGlnLysArgThrLysIle
                                              TTGGGAATCCTGTCTTGGACTGTGTTCTTGTTGTAAGAGGCAAAAA---GGAAAACCC
                                                                             ArglyslysTyrThrIleLeuAspAsnMetAspGluGlnGluArgMetGluLeu
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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/note="HYPOTHETICAL_103.9 KDA PROTEIN homolog [Homo
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97.4%length, match=2763)"
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Please visit our web site for further details.
URL:http://gancome.gsc.riken.jp/
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Location/Qualifiers
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/strain="C57BL/65"
/db_xref="FANTOM_DB:6030408013"
/db_xref="taxon:10090"
/clone="6030408013"
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Neuherberg, GERNANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BWRZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp434C0829) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin,
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434C0829
http://www.rzpd.de/cgi-bin/products/clone and the sequencing project is
available at http://mips.gf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3671 bp mRNA linear HTC 22-SEP-2004 AL834315 MRNA; cDNA DKFZp434C0829 (from clone DKFZp434C0829). AL834315.1 GI:21739924
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3671)
1 (bases 1, A. Mewes, H.W., Weil, B., Amid, C., Osanger, A., Probo, G., Han, M. and Wiemann, S.
                              2538 AGTGAAGCCTGACCAGGAAAAGCAACCTAGTGGAGATCATGGATGTGAACGTCAG
                                                                                            eValPheTyrValGlnSerArgProProPheLysValLeuLysAlaAlaGluValAlaAr
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                                                                         yGlnLeuThrGluGlnArgLysAspThrLeuValArgGlnLeuAlaValLeuLeuAsnVa
              uValGInProAspProArgIysSerGlyLeuValGluLeuThrLeuGlnValGlyValGl
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Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
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Mismatches:
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Acganism="Mus musculus"
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Mus musculus HCM6309 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
                                                               |||::: |||||| :::::: |||
|C28 CAAAACGAGCCTCCCCCCCCCGGATCTTCAAAGGCCATGAGGTGGCAGGAGCTGCTCAAGAGT
GlyCysLeuLeuLysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCysIle
                                                                                                                                                                                                                                                                                                             LysThrLysTyrThrIleLeuAspAsnMetAspGluGluArgMetGluLeuArgPro
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| Aaaagcaagtacaagatcctggatgccacggat---caggaaagcctggaggtgaagcca
                                             GlnSerArgProProPheLysValLeuLysAlaAlaGluValAlaArgAsnLeuHisMet
                                                                                                          ArgieuSeriysGluiysAlaAspPheleuLeuPhelysValleuArgValAspThrAla
                                                                                                                                                                                                                                 CysSerHisLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSerAsn
                                                                                                                                                                                                                                                                                          CysGluTrpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLeuThrGly
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1159 AAACTCCTGCATGGTCAGAATGGCTCTGTACCCAACGGG 2197
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367 rTyr 1020 CTAC	*TYRABNTYrGluTrpAsnLeulleSerHisProThrAspTyrGlnGlyGlulleLysGl 387 	& A	727 sValLeuValLeuProAsnAsnSerIleThrLeu ::-
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1320 GIAC 487 oval :::	GIACCACTGGGAAGAGCTTAAGGGGCCCCTGAGGAGAGAGAG	& 8	847 lleuaspSeraspilelysvaldinlysilearg
	erThrThrAlaAlaLeuIleValAsnAsnAlaValAspTy [III	ර් සි	867 eValPheTyrValGlnSerArgProProPheLye
	lyProAsnHisThrIleThrLeuProGlnAsnSerIleTh	& a	887 gAenLeuHisMetArgLeuSerLysGluLysAla
	GCCCCAACCAASIGAICACCIGCCICAGAACICCAICAC erAspAspHisGlnIleValLeuTyrGluTrpSerLeuGl	& 8	907 gValAspThrAlaGlyCysLeuLeuLysCysSer ::: 2640 AATCAGGACAGTCACATGTCAGGTGAACTGTTCT
	J "H E	\$ B	927 rlysArgCyslleCysSerHisLeuTrpMetGlu
		රු සි	947 pGlyGluSerAsnCysGluTrpSerIlePheTyr :::
607 ngln		중 음	967 eValLeuThrGlyGlyPheThrTrpLeuCyBlle 2820 TGTTGCTTGTCATGGACTACAATC

lecyscyscyslyaargcinlyaargth 987 |||||||||||||||||||||||| rcrgcrgcrgcaaggcaaaa---GG 2876 ||||||| ||||::: | |||||| |||::: |||||::: ||| rggagarcarctrggargrgaacgrcag 2399 AGCCGTACACGGAGCAGAGCACCAAGAT 2519 ::::: ||| | AGCTCTTCAAAGGCCATGAGGTGGCAGC 2579 ACGICATCATIGCCTCTITGICALIGI 2819 NINNINNINNINNINNINNINNINNINNIN 2039 roValGluSerAlaThrLeuAspGlySe 647 yrHisTrpGluHisValArgGlyProSe 667 leAlaThrValThrGlyLeuGlnValGl 687 InglnGlyLeuSerSerThrSerThrLe 707 roProArgAlaArgAlaGlyGlyArgHi 727 euThrAsnLeuValGluGlyValTyrTh 787 laSerAspThrAspThrAlaThrValG1 807 alGluLeuThrLeuGlnValGlyValGl 827 rgAlaHisSerAspLeuSerThrValIl 867 ysvalLeuLysAlaAlaGluValAlaAr 887 laAspPheLeuLeuPheLysValLeuAr 907 luAsnLeuileGlnArgTyrIleTrpAs 947 rvalThrvalLeuAlaPheThrLeuIl 967

267 CTGCCAGGACTCTGCCTGCCATGTCTTTTGGTGGCTAGAAGGGATGTGCATTCAGGCAGA 326 81 rCysProHisLysGluAsnCysGluProLysLysMetGlyProlleArgSerTyrLeuTh 101 827 CTGCAGCAGGCCCCAGAGCTGCCGGGCTTTTAGGACACTCCTCCATTCCATGCTGGT 386 101 rPheValLeuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMetLe 121 101 rPheValLeuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMetLe 121 111 -	121 421 141 453 161	181 uTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsmSerSerValGlyAs 510 C	594 257 648 277 708 291	303 rileprothrPro
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987 rLysIleArgLysLysThrLysTyrThrIleLeuAspAsnMetAspGluGluArgMe 1007	RESULT 8 AV417693 LOCUS LOCUS LOCUS LOCUS AV417693 AV417693 AV417693 ACCESSION AV417693 AV41769	REFERENCE I (Dases 1 to 2962) AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5522), 1960-1963 (2003) REFERENCE 2 (bases 1 to 2962) AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Farikara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Panne M. P. and Cardill M.	TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Sobmitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, COMMENT Rockville, ND 20850, USA COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers 1. 2962 / Organism="Homo sapiens" / Mol type="genomic DNA" / Mol type="genomic DN	Alignment Scores: Pred. No.: 1.176-163

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	aPheGlyGluGlyPheValAsnValThrValLysProAlaArgArgValAsnLeuProPr 434	CCATGGGGGTATGTGAACGTGACAGTCAAGCCAGAGCCCCGTAAGAATCGGCCCCC	434 OVAIATAVAIVALSEEPPOGINLEUGINGINLEUThrLeuthrEethroleuthrearAlaLeuil 454		101 CONTROL OF THE PROPERTY OF	107100470117411741174177777777777777777	Introduction Interpretation Interp	GGGGCLICTANGAGANGAGANGATITICTGANGATACAGCCATATTANAACTANGTANACT	494 UASPPTOGIYASHIYTSETENEATGLEUTHTVAITHTABSSETABGGIYALATHTABNSE 514		1464 TACTACTGCAAACCTGACAACTGAAGCTGTGGAATACCCCCCCTGTGGCCAACGCAGG	vProAsnHisThrIleThrLenDrnGlnAsnSerIleThrLenAsnGlv&snSlnSerSe	CCCCAACCAAGTGATCACCCTGCCCCAAAACTCCATCACCCTCTTTGGGAACCAGAGCAC	554 rhanhanHiaGlnTleVallenffvrGlnFrnSerlenGlvBrnGlvSerGlnGlvIveHi 574		sValValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAs		DTvrThrPheGlnLeuLvsValThrAspSerSerAroGlnGlnSerThrAla***ValTh	:::			634 uLeullePheProValGluSerAlaThrLeuAspGlySerSerSerAspAspHisGl 654	1824 INIXINININININININININININININININININI	654 ylleValPheTyrHisTrpGluHisValArgGlyProSerAlaValGluMetGluAsnIl 674	1884 INWININININININININININININININININININ	674 eAspLysAlalleAlaThrValThrGlyLeuGlnValGlyThrTyrHisPheArgLeuTh 694	1944 INNYINININININININININININININININININI	694 rValLysAspGlnGlnGlyLeuSerSerThrSerThrLeuThrValAlaValLysLysGl 714	2004 NINNINNINNINNINNINNINNINNINNINNINNINNIN	714 uAsnAsnSerProProArgAlaArgAlaGlyGlyArgHisValLeuValLeuProAsnAs 734	2064 AATAAACAACCACCTATAGCCAAGATAACTGGGAATGTGGTGATTACCCTACCCACGAG 2123	nSerIleThrLeuAspGlySerArgSerThrAspAspGlnArgIleValSerTyrLeuTr	CACAGCAGAGCIGGAIGGCICIAAGICCICAGAIGACAAGGGAAIAGICAGCIACCICIG	754 plieArgAspGLyGlnScrProAlaAlaGlyAspVallieAspGLySerAspHisSerVa 774 2184 GAMTGRAGGGAGGGGGGAGGAGGGAGGAGGAGGAGGAGGAGAGAGA	J. J. J. J. J. J. J. J. J. J. J. J. J. J
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Pan troglodytes
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
(Dases 1 to 2962)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrlera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
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Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics
Rockville, MD 20850, USA
This sequence was made by sequencing gethem based on alignment.
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                                                                                                                 2184 GACTCGAGATGAGGGAGCCCAGCAGGAGGGAGGTGTTAAATCACTCTGACCATCACCC
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                                                    714 uAsnAsnSerProProArgAlaArgAlaGlyGlyArgHisValLeuValLeuProAsnAs
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HTC 03-APR-2004

AK049570

Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430042D23 product:HYPOTHETICAL 103.9 KDA PROTEIN homolog [Homo sapiens], full insert sequence.

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishili, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, Y., Izawa, M., Ohara, E., Watahiki, M., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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Direct Submission

L. Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Shipaicaki and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1--22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 220-0045, Japan, (B-mail:genome-reseggeriken:jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Analysis of the mouse transcriptome based on functional annotation
of 60,710 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2189)
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Sciurognathi; Muridae; Murinae; Mus
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Fax:81-45-503-9216)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Rodentia;
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                                                                                Mus musculus (house mouse)
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GI:26340309
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/clone_lib="RIKEN full-length enriched mouse cDNA librar/dev_stage="7 days embryo"
138. ->2189
->2189
/note="unnamed protein product; HYPOTHETICAL 103.9 KDA PROTEIN homolog (Homo sapiens) (SPTR|AAL55781, evidence:FASTY, 85.5%ID, 97.4%length, match=2763)
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Matches:
Conservative:
Mismatches:
Indels:
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db_xref="taxon:]0090"
clone="C430042D23"
                                          organism="Mus musculus"
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
                                                         /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                    codon_start=1
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and

us-10-764-390-3.p2n.rst

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Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, Helix Research Institute.

Location/Qualifiers
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Conservative:
Mismatches:
Indels:
Gaps:
                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP3000279"
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AU130115.1 GI:10990469
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 842)

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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                       aValAlaGlyProAspLysGluLeullePheProValGluSerAlaThrLeuAspGlySe
                                                                                                                                                                                                                                                                                                                                                                                       667 rAlaValGluMetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeuGlnValGl
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pSerAspGlyAlaThrAsnSerThrThrAlaAlaLeuIleValAsnAsnAlaValAspTy
                                                                                          rProProValAlaAsnAlaGlyProAsnHisThrIleThrLeuProGlnAsnSerIleTh
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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AL044313
DKFZp43400729_x1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp43400729_5', mRNA sequence.
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                                                                                     TyrThrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThrAla***ValThr 614
                                                                                                                ValileValGinProGluAsnAsnArgProProValAlaValAlaGlyProAspLysGlu 634
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1 (bases 1 to 597)

Koehrer, Esyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)

Unpublished (1999)
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/clone="Investigated"
/tissue_type="Whole brain"
/dev_stage="", 5, and 15 days newborn"
/dev_stage="", 5, and 15 days newborn"
/dev_stage=""Daylob (TI phage resistant)"
/clone lib="NIH BMAP_GHO"
/clone lib="NIH BMAP_GHO"
/clone lib="NIH BMAP_GHO"
/clone lib="NIH BMAP_GHO"
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/clone lib="NIH BMAP_GHO"
/clone lib="NIH BMAP_GHO"
/clone lib="NIH BMAP_GHO"
/clone lib="NIH BMAP_GHO"
/clone located according to mRNA size fraction, ligated with containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Montal Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                    Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. (1920).

In (bases 1 to 710)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                            CB722905
UI-M-GHO-cef-i-19-0-UI.rl NIH BMAP_GHO Mus musculus cDNA clone
IMAGE:6838844 5', mRNA sequence.
  LeuSerAlaMetGlnGluGlyAspTyrThrPheGln-LeuLysValThrAsp-SerSerA 606
                          606 rgGlnGlnSerThrAla-**ValThr-ValIleValGlnProGluAsnAsn 622
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Mismatches:
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
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Location/Qualifiers
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Mus musculus
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Genome Project.

No s1 sequence available.

This clone (DKPZp43400729) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.

Location/Qualifiers
                                                             1. .597

/organism="Homo sapiens"

/mol_type="memoral"

/db_xrel=taxon:9606"

/clone="DKFZp44400729"

/tissue_type="testis"

/dev_stage="adult"

/lab_host="BH108"

/clone_lbh="434 (synonym: htes3)"

/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
                                                                                                                                                                                                                                                                                                                                             GACTCGGACGGAGCCACTAACTCTACAACTGCAGCCCTAATAGTGAACAATGCTGTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTITGAATGGAAACCAGAGCAGTGACGATCACCAGATTGTCCTCTATGAGTGGTCCCTG
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Best Local Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamahia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 599)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizuhima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukishms.u-tokyo.ac.jp.
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/clone="FBR04757"
/tisque_type="brain"
/dew stage="fetal"
/clone_lib="Sugano cDNA library, fetal brain"
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Matches:
Conservative:
Mismatches:
Indels:
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                                              Homo sapiens (human)
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                                                                                                                         542 GCAGGCCCCAACCAAGTGATCACCCTGCCTCAAAACTCCATCACCCTTTTGGGAATCAG
                                                                                                                                                                                         SerSerAspAspHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySerGluGly
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                             602 AACTCTACCACTGCAAGCCTGACTGTGAACAAAGCTGTGGATTACCCTCCTGTGGCCAAT
                                                                                                533 AlaGlyProAsnHisThrIleThrLeuProGlnAsnSerIleThrLeuAsnGlyAsnGln
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1 (bases 1 to 842)

2 Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.

2 Porcine EST collection using a normalized library constructed from embryos representing early developmental stages

3 Contact: Smith TPL

4 Contact: Smith TPL

5 USDA, ARS, US Meat Animal Research Center

6 Dox 166, Clay Center, NE 68933-0166, USA

7 Tel: 402 762 4366

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/db xref="taxon:9823"
/tisher_type="pooled"
/lab host="DHIOB"
/clone_lib="MARC 4PIG"
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/ibrary made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
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                                                                                                                                                                                            CK463785 842 bp mRNA linear
934714 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
Query Match:
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ORGANISM
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Adro0858 Human 254
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Adm36226 Murine SS
Adi21796 Novel hum
Aadi1067 Human sec
Adf42453 Human sec
Adf42453 Human SC
Aah18563 Human SC
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Abl13095 Drosophil
Aah06733 Human CDN
Aas673181 DNA encod
Abl13094 Drosophil
Aah06733 Human cDN
Aas6915 Human adi
Aah09021 Human bon
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Aac69580 Human sec
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Add17315 Human ben
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Abz7634 Nucleotid
Add3637 DNA encod
Add3637 DNA encod
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254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
254P1D6B v.2; gene; 88; chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 254P1D6B v.2 encoding cDNA SEQ ID NO:4.
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ADN46464 16
ADN47960 04
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512. .3730
/*tag= a
/product= "254PlD6B v.2"
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ADN4 6123
                      ADM36226
ADI21796
AADI1067
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AAH89908
ADG15051
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ACA25573
ABA21464
ADQ89963
AAS05390
ABK64829
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ABL13094
AAH06733
ACA56915
AAH90021
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AAVS8761
ABL13095
AAH15983
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    Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/Cogl_1/USPTO=pool_p/USIO764390/runat 12102005 110203_22319/app_query.fasta_1.1223
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Adr00591 Human 2
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                                                                                                                                                                                                                                                     8780412
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                       nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                    of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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ADR00860
ADR00859
ADR00595
                                                                             October 12, 2005, 10:29:21
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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81 SerCysProHisLysGluAsnCysGluProLysLysMetGlyProIleArgSerTyrLeu 100

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Challita-Eid PM, Jakobovits A, Kanner SB, Raitano AB, Ja Perez-Villar JJ, Faris M; 2004-580991/56 (AGEN-) AGENSYS INC P-PSDB; ADR00594

New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Claim 10; SEQ ID NO 4; 345pp; English.

The present invention describes a 254P1D6B small interfering RNA (51RNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254P1D6B protein, or corresponds to a subsequence of the occess the composition that comprises, consists assembled. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADR00592. ADR00594 or ADR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein contact is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98 homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein or a citat encodes the protein; (3) a composition that modulates the composition that comprises the composition that modulates the castum of a call that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human cut unit transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and con-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and con-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and concerned to a servival of cancer cells that expresses the protein of P1; and concerned expresses the protein of P1; and concerned expresses the protein of P1; and concerned expresses the protein of P1; 254P1D6B has cytostatic activity, and can be used in the exemplification of the present concerned by a concerned by the composition of the presen

Sequence 6791 BP; 1812 A; 1542 C; 1684 G; 1753 T; 0 U; 0 Other;

512 ATGGCGCCCCCACAGGTGTGCTCTTCATTGCTGCTGCTGGTGACAATTGCAGGTTGT 571 572 GCCCGTAAGCAGTGCAGCGAGGGAGACATATTCCAATGCAGTCATTTCACCTAACTTG 631 691 751 21 AlaArgiysGlnCysSerGluGlyArgThrTyrSerAsnAlaValileSerProAsnLeu 40 41 GluThrThrArglleMetArgValSerHisThrPheProValValAspCysThrAlaAla 60 80 1 MetAlaProProThrGlyValLeuSerSerLeuLeuLeuLeuValThrIleAlaGlyCys 20 CysCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuVal TGCTGTGACCTGTCCAGCTGTGACCTGGCCTGGTTCGAGGGCCGCTGCTACCTGGTG GAAACCACCAGAATCATGCGGGTGTCTCACACCTTCCCTGTCGTAGACTGCACGCCGCT 6791 1069 Length: Matches: Conservative: Mismatches: Indels: US-10-764-390-3 (1-1072) x ADR00593 (1-6791) 5574.00 99.72% 99.72% Best Local Similarity: Percent Similarity: Alignment Scores: 61 Query Match: à 셤 ð a 8 g ઠે

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2	70/	SCCCCACACACACACT GT GAGCCCCAAGAAGAT GGGCCCCATCAGGTCTTATCTC
ò	101	ThrPheValLeuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMet 120
QQ	812	rieriecrecedecterricadadecerecadaderecederadadedecareare
ć	121	LeukanargGlySerProSerGlyIleTrpGlyAapSerProGlukapIleArgLyaAsp 140
qq	872	cededatchededeactcacchedeatatcagaaagaac 93
δ	141	***PheLeuGlyLysAspTrpGlyLeuGluGluMetSerGluTyr***AspAspTyr 16
qq	932	tttctaggcaaagattggggcctagaggagatgtctgagtacgcagatgacta
ò	161	ArgGluLeuGluLysAspLeuLeuGlnProSerGlyLysGlnGluProArgGlySerAla 180
QQ	992	GAAGCTGGAAAGGACCTCTTGCAACCCAGTGGCAAGCAGGAGCCCAGAGGAAGTGC
ò	181	
qq	1052	GAGTACACGGACTGGGGCCTACTGCCGGGCGAGGGGGGCCTTCAACTCCTCTGTTGGA 1111
ò	201	
Ωp	1112	GÁCAGTCCTGCGGTGCCAGCGGAGGACGCAGGACCCTGAGCTCCATTACCTGAATGAG 1171
ò	221	_
ф	1172	rcéécticaaccectáccecaaaacicecteagadaagagitetricetrecegaer 1231
ò	241	ThrProSerSerGlyGluValLeuGluLysGluLysBlaSerGlnLeuGlnGluGlnSer 260
ΟD	1232	ACTCCATCTTCAGGAGAGGGTGTTGGAGAAAGAAAGGCTTCTCAGCTCCAGGAACAATCC 1291
à	261	SerAsnSerSerGlyLysGluValLeuMetProSerHisSerLeuProProAlaSerLeu 280
QQ	1292	AGCAACAGCTCTGGAAAAGAGGTTCTAATGCCTTCCCATAGTCTTCCTCCGGCAAGGCCTG 1351
ò	281	GluLeuSerSerValThrValGlulysSerProValLeuThrValThrProGlySerThr 300
op QC	1352	LAGCTCAGCGTGGAGAAAGCCCAGTGCTCACAGTCACCCGGGGAGTACA 14
à	301	hrProSerGlu 32
q	1412	.AGCATCCCAACACTCCCACTAGCGCAGCCCCCTCTGAGTCCACCCCATCTGAG 14
ò	321	
QQ	1472	
ò	341	alAlaPro 36
DР	1532	GATAACCTAATTATAACTTTACCCGACAATGAAGTTGAACTGAAGGCCTTTGTTGCGCCA 1591
ò	361	
Dp	1592	GCGCCACCTGTAGAACAACCTACAACTATGAATGGAATTTAATAAGCCACCCCACAGAC 1651
ò	381	
qq	1652	TACCAAGGTGAAATAAAACAAGGACACAAGCAAACTCTTAACCTCTCTCT
λ̈́o	401	GlyLeuTyrValPheLysValThrValSerSerGluAsnAlaPheGlyGluGlyPheVal 420
셤	1712	
ò	421	
đ	1772	
ò	441	GlnLeuGlnGluLeuThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThr 460

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254P1D6B protein, or corresponds to a subsequence of the occess the consists acid open reading frame (ORF) sequence which encodes the consists assentially of or consists of a peptide of eight, nine, ten, or eleven contiguous anino acids of a protein of figure 2 [R1, see SRQ ID NO.3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein CC that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 98 homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide comprising a polynucleotide contact in a sample, the presence of a 254P1D6P-related protein or a 254P1D6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition described above; (1) a pharmacentical confidence or a diagnostic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent confidence in gene protein of P1; (7) a pharmacentical confidence or a diagnostic agent to a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent confidence the protein of P1; (12) inhibiting growth, reproduction or survival of cancer cells that expresses the protein of P1; and cust in a gene full composition and methods are useful and election and present and described and methods are useful to survival or ancertain and described and election or survival of cancer cells the human control and described and methods are useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New 254PID6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PID6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                         Jakobovits A, Challita-Eid PM,
                        /transl_except= (pos:935. .937,aa:Xaa)
/transl_except= (pos:980. .982,aa:Xaa)
/transl_except= (pos:245. .2347,aa:Xaa)
/note= "Xaa is any amino acid"
product= "254P1D6B v.1 clone LCP-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; SEQ ID NO 2; 345pp; English.
                                                                                                                                                                                                                                     23-JAN-2004; 2004WO-US001965
                                                                                                                                                                                                                                                                                24-JAN-2003; 2003US-0442526P
                                                                                                                                                                                                                                                                                                                                                                                                    Perez-Villar JJ, Faris M;
                                                                                                                                                                                                                                                                                                                                                                            Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating cancer.
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                                                                                                                                                                                                                                                                                                                              (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ADR00592.
                                                                                                                                           WO2004067716-A2
                                                                                                                                                                                       12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                              Kanner SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
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3 8 for treating and detecting cancer. The present sequence encodes the human 254PID6B v.1 clone LCP-3, which is used in the exemplification of the present invention. The human 254PID6B gene is located on chromosome 6p22.

Sequence 6791 BP; 1809 A; 1537 C; 1677 G; 1751 T; 0 U; 17 Other;

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: 99.91% Ouery Match: 13	0 5574.00 99.91% 99.91% 19.89%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	6791 1071 0 1 0 0 0
OS-10-764-590-3 (1-10/2) X ALKOUSSI (1-6/31) Qy	hrGlyValLeuS	erSerLeuLeuLeuI 	1 MetalaproproThrGlyValLeuSerSerLeuLeuLeuLeuValThrIleAlaGlyCyg 20

1111 GAGCTCAGCTCAGCTCACCGTGGAGAAAAGCCCAGTGCTCACACTCACCCCGGGGAGTACA 1411 992 ceseaaccrecadaaceaccrerrecaacceacreceaseaceaseaceaseaceaseseasece 1051 280 300 361 AlaProProValGluThrThrTyrAsnTyrGluTrpAsnLeuIleSerHisProThrAsp 380 100 871 140 240 260 691 811 120 160 991 180 200 631 751 9 80 40 GluLeuSerSerValThrValGluLysSerProValLeuThrValThrProGlySerThr GluHisSerIleProThrProProThrSerAlaAlaProSerGluSerThrProSerGlu LeuProlleSerProThrThrAlaProArgThrValLysGluLeuThrValSerAlaGly AspAsnLeullelleThrLeuProAspAsnGluValGluLeuLysAlaPheValAlaPro ACTITITETGCTCCGGCCTGTTCAGAGGCCTGCACAGCTGCTGGACTATGGGGACATGATG LeuAsnArgGlySerProSerGlyIleTrpGlyAspSerProGluAspIleArgLysAsp CTGAACAGGGGCTCCCCCTCGGGGATCTGGGGGGACTCACCTGAGGATATCAGAAAGGAC Leu***PheLeuGlyLyBAspTrpGlyLeuGluGluMetSerGluTyr***AspAspTyr 161 ArgGluLeuGluLysAspLeuLeuGlnProSerGlyLysGlnGluProArgGlySerAla 1052 GAGTACACGGACTGGGGCCTACTGCCGGGCAGGGGGGGGCCTTCAACTCCTCTGTTGGA SerAlaSerThrProAlaProLysLeuProGluArgSerValLeuLeuProLeuProThr TCGGCTTCAACCCCTGCCCCAAAACTCCCTGAGAAGTGTGTTGCTTCCCTTGCCGACT ThrProSerSerGlyGluValLeuGluLysGluLysAlaSerGlnLeuGlnGluGlnSer SerAsnSerSerGlyLysGluValLeuMetProSerHisSerLeuProProAlaSerLeu 512 ATGGCGCCCCCACAGGTGTGCTCTTTTTTTGCTGCTGCTGGTGACAATTGCAGGTTGT GluThrThrArgIleMetArgValSerHisThrPheProValValAspCysThrAlaAla CysCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuVal SerCysProHisLysGluAsnCysGluProLysLysMetGlyProIleArgSerTyrLeu AGCTGCCCCCACAAGAGAACTGTGAGCCCAAGAAGATGGGCCCCCATCAGGTCTTATCTC ThrPheValLeuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMet 932 TTGMCCTTTCTAGGCAAAGATTGGGGCCTAGAGGAGATGTCTGAGTACKCAGATGACTAC GluTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsnSerSerValGly AspSerProAlaValProAlaGluThrGlnGlnAspProGluLeuHisTyrLeuAsnGlu 21 AlaArgLysGlnCysSerGluGlyArgThrTyrSerAsnAlaValIleSerProAsnLeu 872 221 1172 1232 1352 1412 181 241 261 281 301 321 341 752 812 121 141 201 692 81 101 41 61 셤 a g g ò g ò 셤 ઠ 셤 Š g ઠે g ઠ 셤 8 셤 ò 셤 8 셤 ð d a 셤 a Š ઠે Š ð 8 ò

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The present invention describes a 254P1D6B small interfering RNA (SiRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254P1D6B protein, or corresponds to a subsequence of the codes the computation of stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists essentially of, or consists of a peptide of eight, nine, ten, or consists essentially of, or consists of a peptide of eight, nine, ten, or cleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00595), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein CC that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99, homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of P1; (5) generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254P1D6B-related protein or a 254P1D6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition described above; in a human continuant transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and continual described above in a human continual that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and continual detecting growth, reproduction or survival of cancer cells that express the protein of P1: 254P1D6B has cytostatic activity, and can be useful growth, reproduction or survival of cancer cells the human 254P1D6B v.3 nucleotide sequence, which is used in the present invention. The human 254P1D6B errores the protein of the present invention. The human 254P1D6B errores the protein of protein or surviv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New 254PID6B SIRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PID6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                                                         254PID6B-related protein; cytostatic; gene therapy; cancer; human;
254PID6B v.3; chromosome 6; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Challita-Eid PM,
                                                                                                                   254P1D6B; small interfering RNA; siRNA; immune response;
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                                                                   Human 254P1D6B v.3 nucleotide sequence SEQ ID NO:271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; SEQ ID NO 271; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jakobovits A,
                                                                                                                                                                                                                                                                                                                                                            23-JAN-2004; 2004WO-US001965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kanner SB, Raitano AB, J
Perez-Villar JJ, Faris M;
                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       located on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-580991/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                            WO2004067716-A2.
                                                                                                                                                                                                                  Homo sapiens.
                      04-NOV-2004
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6797 1069 0 3 2 Length:
Matches:
Conservative:
Mismatches: 0 5546.50 99.53% 99.53% Alignment Scores:

Percent Similarity: Best Local Similarity: Query Match: DB:

1413 1533 1174 TGAGTCGGCTTCAACCCCTGCCCCAAAACTCCCTGAGAGAAGAGGTGTTGCTTCCCTTGCC 1233 ATCCAGCAACAACAACTCTGGAAAAGAAGATCTAATGCCTTCCCATAGTCTTCCTCCGGCAAG 1353 994 cracceceaecrecadadeaccrerrecaacceaerecaaecaaecaecaecaecaecaeaea 1053 1234 gacracriccarcricaggagagagargringgagaaagaaaaggcricticagcriccaggaaca 1293 239 319 aGlyAspAsnLeullelleThrLeuProAspAsnGluValGluLeuLysAlaPheValAl 359 813 119 573 633 693 753 159 GGACTTGCCCTTTCTAGGCAAAGATTGGGGCCTAGAGAAGATGTCTGAGTACTCAGATGA 993 pTyrArgGluLeuGluLygAgpLeuLeuGlnProSerGlyLysGlnGluProArgGlySe 179 ralaGluTyrThrAspTrpGlyLeuLeuProGlySerGluGlyAlaPheAsnSerSerVa 199 79 66 39 1354 ccrosactcactcactcacceresaaaagcccagrecreacagreacceessag nSerSerAsnSerSerGlyLysGluValLeuWetProSerHisSerLeuProProAlaSe rThrGluHisSerIleProThrProProThrSerAlaAlaProSerGluSerThrProSe rGluLeuProlleSerProThrThrAlaProArgThrValLysGluLeuThrValSerAl YCYSAlaArgLysGlnCysSerGluGlyArgThrTyrSerAsnAlaValIleSerProAs rLeuThrPheValLeuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMe 814 rereacritificacrececeretreacaccrecececaccaccrececacacat 8AspLeu***PheLeuGlyLysAspTrpGlyLeuGluGluMetSerGluTyr***AspAs 1GlyAspSerProAlaValProAlaGluThrGlnGlnAspProGluLeuHisTyrLeuAs nGluSerAlaSerThrProAlaProLysLeuProGluArgSerValLeuLeuProLeuPr rLeuGluLeuSerSerValThrValGluLysSerProValLeuThrValThrProGlySe 514 ATGGCGCCCCCACACAGGTGTGCTCTCTTCATTGCTGCTGCTGGTGACAATTGCAGTTTGG 574 Trerececeraageagrecagegagegagegacaratrecaargeagrearrecaaa nLeuGluThrThrArgIleMetArgValSerHisThrPheProValValAspCysThrAl aAlaCysCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLe tMetLeuAsnArgGlySerProSerGlyIleTrpGlyAspSerProGluAspIleArgLy oThrThrProSerSerGlyGluValLeuGluLysGluLysAlaSerGlnLeuGlnGluGl uValSerCysProHisLysGluAsnCysGluProLysLysMetGlyProIleArgSerTy US-10-764-390-3 (1-1072) x ADR00860 (1-6797) 1054 199 1114 239 1294 39 874 934 259 319 339 Н 13 29 694 79 66 119 139 159 179 219 279 299 유 g 원 셤 ò 셤 ઠ g ð 셤 ò 요 à g ò 셤 à 셤 ઠે 유 ઠ 요 ઠે 셤 ò 원 à ò g ð 8 Š 셤 ઠે δ

719 OArgAlaArgAlaGlyGlyArgHisValLeuValLeuProAsnAsnSerIleThrLeuAs 739 2674 CAGGGCCGGGCGGCAGACATGTTCTTGTGCTTTCCATAATTCCATAATTCCATTACTTTGGA 2733 2734 DGLySerArgSerThrSphapGlnArg1leValSerTytLeuTpilleArgAspG1yG1 759 1	779 rAsiLeuValGluGlyValTyrThrPheHisLeuArgValThrAspSerGlnGlyAlase 799 179 rAsiLeuValGluGlyAlase 799 1	839 9GInLeuAlaValLeuLeuAsnValLeuAspSerAspIleLysValGInLysIleArgAl 859	999 pPheLeuLeuPheLysValleuArgValAspThrAlaGlyCysLeuLeuLysCysSerGl 9	3334 CCTTATACAGGGTTATATCTGGGATGGAGGGGGGTGGTGGTGGTGGTGGTGGTGGTGGT	999 pasnMetAspGluGlnGluArgMetGluLeuArgProLysTyrGJyllelysHisArgSe 1019
1534 TGGAGATAACCTAATTATAACTTTACCCGACAATGAAGTTGAACTGGAAGGCCTTTGTTGC 1593	JAMIN 17 Valse 43 CHIN 18 STITC 18 SINSE 45 CAAAG 18	TACAGATGATACTGAAATAGTGAGTTATCATTGGGAAGAAATAAACGGGCCCTTCATAGA 1953	ACCAT 2133 Gln11 559 [CAGAT 2193 GlnG1 579 CAGGG 2253		TyrHi

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to composition that comprises a double stranded siRNA that corresponds to a subsequence which encodes the corresponds to a subsequence of the overwhere the couple stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists assentially of or consists (1) a composition that comprises, consists essentially of, or consists (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADRO0592, ADRO0594 or ADRO0596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein cot that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 93k homologous or identical to an entire amino acid sequence of P1; (2) a polymuclectide that is a full complement of the polymuclectide described above; (4) constraints in a sample, the presence of a 254P1D6B-related protein or a conference of a 254P1D6B-related protein or a composition that comprises the composition that modulates the composition that comprises the composition described above; (10) a non-human transgenic animal that produces the antibody; (11) delivering a cytocytic agent or a diagnostic agent to a cell that expresses the protein of P1; (7) a pharmaceutical conference of a protein of caperating and detecting growth, reproduction or survival of cancer cells that express the protein of P1. 254P1D6B has cytostatic activity, and can be useful for treating and detecting cancer. The present expressents the protein of P1. Conference of the present sequence represents the composition of the present invention. The human 254P1D6B are useful. The present invention. The human 254P1D6B are useful.
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                                                                                                                                                                                         254PID6B; small interfering RNA; siRNA; immune response;
254PID6B-related protein; cytostatic; gene therapy; cancer; human;
254PID6B v.1; chromosome 6; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Challita-Eid PM,
                                                                                                                                                 Human 254PlD6B v.1 nucleotide sequence SEQ ID NO:270
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                      ADR00859 standard; DNA; 6797 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perez-Villar JJ, Faris M;
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ADR00859
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1174 TGAGTCGGCTTCAACCCCTGCCCCAAAACTCCCTGAGAAGTGTGTTGCTTCCCTTGCC 1233
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1174 TORACTARCCANANCTICCACCACCACCACCACCACCACCACCACCACCACCACCA

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The present invention describes a 254PIDGB small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to composition that comprises a double stranded siRNA that corresponds to a subsequence which encodes the case in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P., see SEQ ID NO:3, 5 or 7 ADRO6592, ADRO6594 or ADRO6596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein contact is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or dentical to an entire amino acid sequence of PI; (2) a polymucleotide that is a full complement of the polymucleotide described above, (4) dentical in a sample, the presence of RI; (2) a polymucleotide chart is a full complement of the polymucleotide described above, (4) detecting in a sample, the presence of a 254PID6B-related protein or a 254PID6B-related protein or a 254PID6B-related protein or a composition that modulates the composition that modulates the composition that comprises the composition that modulates the composition that comprises the composition described above in a human transgenic animal that produces the antibody; (1) a pharmaceutical corrections to a diagnostic agent to a cell that expresses the protein of P1; and hybridoma that produces the antibody; (1) a correction of a diagnostic agent to a cell that expresses the protein of P1; and C12 inhibiting growth, reproduction or survival of cancer cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                              254PID6B-related protein, cytostatic; gene therapy; cancer; human; 254PID6B v.3; gene; ss; chromosome 6.
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                                                                                                                                                                                                                                                                                            254P1D6B; small interfering RNA; siRNA; immune response;
eArgAsnGlyAlaSerPheSerTyrCysSerLysAspArg 1072
                     3694 CAGAAATGGAGCTTCCTTCAGTTATTGCTCAAAGGACAGA 3733
                                                                                                                                                                                                                                                   Human 254PlD6B v.3 encoding cDNA SEQ ID NO:6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "254P1D6B v.3"
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                                                                                                                         ADR00595 standard; cDNA; 6991
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            used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence enrodes the human 25471D6B v.3, which is used in the exemplification of the present invention. The human 254P1D6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                             681 TTATGGTGGATGCACTCATGGCAAAAAATCACTGGTGAGCATCATTTAAGAAGACCCAT 740
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express the protein of P1. 254P1D6B has cytostatic activity, and can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 254PlD6B v.3 transcript variant nucleotide sequence SEQ ID NO:269.
3621 AGGAGGTTTCACTTGGCTTTTGCATCTGCTGCTGCAAAAGACAAAAAAGACAAAAAAGGACTAAAAATCAG
                                                             3741 GCCCAAATATGGTATCAAGCACCGAAGCACAGAGCACAAGCACACACTCCAGCCTGATGGTATCCGA
                                                                                                                                                                                      1050 nProLysValSerMetAsnGlySerIleArgAsnGlyAlaSerPheSerTyrCysSerLy
                                                                                                           gProLysTyrGly1leLysHisArgSerThrGluHisAsnSerSerLeuMetValSerGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254PlD6B-related protein; cytostatic; gene therapy; cancer; human; 254PlD6B v.3; chromosome 6; gene; ds.
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that is a full complement of the polymucleotide described above, (4) generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PiD6B-related polymucleotide, (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hyridoma that produces the antibody; (10) a non-human transgenic animal that expresses the protein of P1; and class the protein of P1; 254PID6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful cor treating and detecting cancer. The present sequence represents the human 254PID6B v.3 transcript variant nucleotide sequence, which is used in the exemplification of the present invention. The human 254PID6B gene
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(3) a composition comprising a polynucleotide
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550 yAanGlnSerSerAspAspHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySe 570 	570 rGluGlyLysHisValValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMe 590 	590 tGlnGluGlyAspTyrThrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerTh 610 	o -i	630 yProApplysGluLeuilePheProValGluSerAlaThrLeuAppGlySerSerSerSe 650 	650 rAspaspHisGlylleValPheTyrHisTrpGluHisValArgGlyProSerAlaValGl 670 	670 uMetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeuGlnValGlyThrTyrHi 690 	690 BPheargLeuThrVallysAspGlnGlnGlnGlyLeuSerSerThrSerThrLeuThrValal 710 	710 aValLysbysGluasnasnSerProProArgalaargalaGlyGlyargHisValLeuVa 730 	730 lLeuProAsnAsnSerIleThrLeuAspGlySerArgSerThrAspAspGlnArgIleVa 750 	750 SertytleuTrplleArgAspGlyGlnSerProAlaAlaGlyAspVall1eAspGlySe 770	servalalateuGlnteuT 	serdingiyalaserAspThrAspThrAlaThrValGluValG 	0 oAspProArgiysSerGlyLeuValGluLeuThrLeuGlnValGlyValGlyGlnLeuTh 83 	830 rGluGlnArgLysAspThrLeuValArgGlnLeuAlaValLeuLeuAspse 850 	850 rAspileLysValGlnLysileArgAlaHisSerAspLeuSerThrValileValPheTy 870 	870 rValGinSerArgProProPheLysValLeuLysAlaAlaGluValAlaArgAsnLeuHi 890	890 8MetArgLeuSerLysGluLysAlaAspPheLeuLeuPheLysValLeuArgValAspTh 910
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1221 CAGTGGCAAGCAGGAGCCCAGAGGGAGTGCCGAGTACACGGACTGGGGCCTACTGCCGGG 1280 190 ySerGluGlyAlaPheAsnSerSerValGlyAspSerProAlaValProAlaGluThrGl 210		OGIUARGSerValLeuLeuProLeuProThrThrProSerSerGlyGluValLeuGluLy	250 sGluLysAlaSerGlnLeuGlnGluGlnSerSerAsnSerSerGlyLysGluValLeuWe 270	270 tProSerHisSerLeuProProAlaSerLeuGluLeuSerSerValThrValGluLysSe 290	ProValleuThrValThrProGlySerThrGluHisSerIleProThrProProThrSe 	310 rAlaAlaProSerGluSerThrProSerGluLeuProIleSerProThrThrAlaProAr 330	9ThrValLy8GluLeuThrValSerAlaGlyAspAsnLeuIleIleThrLeuPrOAspAs 	IN		390 sGlnthrLeuAsnLeuSerGlnLeuSerValGlyLeuTyrValPheLysValThrValSe 410 	rSerGluAsnAlaPheGlyGluGlyPheValAsnValThrValLysProAlaArgArgVa 	430 lAsnLeuproprovalAlavalValSerProGlnLeuGlnGluLeuThrLeuProLeuTh 450 	450 rSerAlaLeuIleAspGlySerGlnSerThrAspAspThrGluIleValSerTyrHisTr 470 	470 pGluGlu1leAsnGlyProPhe1leGluGluLysThrSerValAspSerProValLeuAr 490 	gleuserasnleuaspproglyasnlyrserbheargleulhrvalthraspseraspol 	yAlaThrAsnSerThrThrAlaAlaLeulleValAsnAsnAlaValAspTyrProProVa	AlaasaalagiyroasahisThrileThrieuProglaasaserileThrieuasagi

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                                                                                           970
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               3441 AGCAGGTTGCCTTCTGAAGTGTTCTGGCCATGGTCACTGCGACCCCCTCACAAAGGGCTG
                                                           CATTTGCTCTCACTTATGGATGGAGAACCTTATACAGGGTTATATATCTGGGATGGAGAGAG
                                                                                                        CAACTGTGAGTGGAGTATATTCTATGTGACAGTGTTGGCTTTTACTCTTATTGTGCTAAC
                                                                                                                                                         AGGAGGTTTCACTTGGCTTTTGCATCTGCTGCTAAAAGACAAAAAAGGACTAAAATCAG
                                                                                                                                                                                gLysLysThrLysTyrThrIleLeuAspAsnMetAspGluGluGluArgMetGluLeuAr
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                                               sileCysSerHisLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSe
                                                                                           rAsnCysGluTrpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLeuTh
                                                                                                                                       rGlyGlyPheThrTrpLeuCyslleCysCysCysLysArgGlnLysArgThrLyslleAr
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2002US-0373824P.
2002US-0377883P.
2002US-0383218P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human SECP-27 cDNA
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19-APR-2002;
03-MAY-2002;
24-MAY-2002;
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The invention relates to a novel isolated SECP (secreted protein)

Complexity, relaxant, antithyroid, antidiabetic, cytostatic,
dermatological, immunosuppressive, antiinflammatory, thyromimetic,
dermatological, immunosuppressive, antiinflammatory, thyromimetic,
antiallergic, cerebroprotective, gastrointestinal, hepatotropic,
antiallergic, anticonvulsant, antiparkinsonian, antibacterial,
compliant anticonvulsant, antiparkinsonian, antibacterial,
antiparasitic, fungicide, protozoacide, virucide, uropathic,
antirheumatic, cardiant, cardiovascular, anti-HIV and nootropic
antirheumatic, cardiant, cardiovascular, anti-HIV and nootropic
contivities. The polypeptide may be useful in diagnosing, preventing and
treating disorders including neurodegenerative disorders such as
cortivities. The polypeptide may be useful in diagnosing, preventing
compounce dystrophy and catatoria, endocrine disorders particularly
cdiabetes and Grave's disease, cancers such as leukaemia, cervical or
breast cancer, immunological disorders including scleroderma, systemic
competent infections particularly viral, bacterial, fungal, parasitic,
competed infections particularly viral, bacterial, fungal, parasitic,
and hepatic diseases particularly cirrhosis. The polymucleotides may be
context therapy procedures. The current sequence is that of the human SECP cDNA
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Marquis JP, Lee SY, Elliott VS, Ramkumar J, Hafalia AJA;
Kable AE, Chawla NK, Emerling BM, Khare R, Jiang X, Jackson AA;
Hawkins PR, Jin P, Mason PW, Richardson TW, Swarnakar A, Lal PG;
Warren BA, Lee S, Griffin JA, Fu GK, Wilson AD, Xu Y, Bulloch SA;
Becha SD, Bhatia UG, Burrill JD, Blake JJ, Ho A, Zheng W;
                                                                                                                                                                                                                                                                                     New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCGTAAGCAGTGCAGCGAGGGAGGACATATTCCAATGCAGTCATTTCACCTAACTTG
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Matches:
Conservative:
Mismatches:
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96.83*
96.02*
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                                                                                                                                                                                                                                   P-PSDB; ADG14994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3808
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DB:
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CysCysAspLeuSerSerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuVal

187 61

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101 ThrPheValLeuArgProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMet 120		TTGCCCTTTCTAGGCAAGATTGGGGCCTAGAGGAGTGCTGAGTACTCAGATGACTAC	200	Qy AspSerProAlaValProAlaGluThxGlnGlnAspProGluLeuHisTyrLeuAsnGlu 220		Oy ThrProSerSerGlyGluValLeuGluLysGluLysAlaSerGlnLeuGlnGluGlnSer 260	Qy SerAenSerSerGlyLysGluValLeuMetProSerLisSerLeuProProAlaSerLeu 280	Qy		340 1086	Qy AsphenLeullelleThrLeuProAsphanGluValGluLeuLysAlaPheValAlaPro 360 [1]			420			CAACIGCAAGAGCICACITIGACGICAGCCCICATIGATGGCAGCCAAAGTACA 1990 Qy AspAspThrGluileValSerTyrHisTrpGluGluIleAsnGlyProPheIleGluGlu 480

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LeuGluGluMetSerGluTyr***AspAspTyrArgGluLeuGluLysAspLeuLeuGln 169
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Best Local Similarity:
                                Matsuzawa Y,
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This invention relates to novel membrane proteins that are associated with differentiation and/or metabolic function of adipocytes, in particular of mouse origin. Specifically, it refers to the isolated nucleic acid molecules encoding all or part of these proteins, appropriate antibodies and screening assays useful for the development of drug compositions derived thereof. The present invention describes these compositions as useful for the treatment of diseases associated with abnormalities of adipocyte function, such that they can be used to prevent, treat or diagnose obesity, hypertension, hyperlipsemia, diabetes and arteriosclerosis. Accordingly, they exhibit anorectic, antidiabetic, antianteriosclerosic, antilipsemic and hypotensive activities. This
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                                                                                                                                                                                                           Mouse membrane and secretory proteins of adipocyte origin and polynucleotides encoding them for screening compounds as remedies foobssity, diabetes, arteriosclerosis, hypertension and hyperlipemia.
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gAsnLeuHisMetArgLeuSerLysGluLysAlaAspPheLeuLeuPheLysValLeuAr 907
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           rLysArgCyslleCysSerHisLeuTrpMetGluAsnLeulleGlnArgTyrlleTrpAs
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3 G, Zhou P,
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Ghosh M, Xue AJ, Wehrman T, Weng
Haley-Vicente D;
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13-SEP-2002; 2002US-00323739.
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WPI; 2003-354603/33. P-PSDB; ADI21080.

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The invention relates to an isolated polymucleotide encoding a polympetide with biological activity. The polymucleotides and polympetides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polymocleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising mathbodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or cegeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents CDNA encoding a novel human protein.
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                       rLygGluLygAlaAspPheLeuLeuPheLygValLeuArgValAspThrAlaGlyCysLe 914
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                                             sTyrThr1leLeuAspAsnMetAspGluGlnGluArgMetGluLeuArgPro----Ly
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10-JAN-2001; 2001WO-US000895.

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The invention relates to human secreted proteins (SECP) and nucleic acid molecules encoding such proteins. SECP agonist and/or antagonist is useful for treating diseases associated with decreased expression or overexpression of functional SECP. The disorders treated include cell proliferative disorders such as cancer, arteriosclerosis, although such as capaired immune deficiency syndrome confirmancy disorders such as acquired immune deficiency syndrome (AIDS), allergies, anaemia, asthma, autoimmune thyroiditis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome, Grave's disease, comultiple sclerosis, mysethenia gravis, pancreatitis, uvetis, Werner syndrome and infections; cardiovascular disorders such as congestive heart failure, myocardial infarction, ischaemic heart disease and angina pectoris; neurological disorders such as stroke, Huntington's disease, Alzheimer's disease, Pick's disease, epilepsy, dementia, and Parkinson's disease, and developmental disorders such as renal tubular acidosis and cushing's syndrome. SECP DNA is useful to create knock-in humanised containing genomic sequence, and an and in mile of the naturally cocurring genomic sequence, and in molecular biological techniques. The process of the second of the condition of the naturally conserved of the condition of the condition of the naturally conserved of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condi
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                                                                                                                                                                                                                                                                                                                                           Au-Young J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated human secreted protein useful for diagnosing, preventing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological and developmental disorders.
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Lu DAM, Yang J, Burford N, A
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AATAGGACAGGCGCACTGCTCAAGTGAC 1969 OPTOVAIAIAVAIAIAGIYPTOABDLYBGI 634 AABDGIySerSerSerAspAspHisGl 654 GGIyProSerAlaValGluMetGluAsnIl 674 uGlnvalGlyrhrTyrHisPheArgLeurh 694 rSerThrLeuThrValAlaVallySLySG1 714 yAspvallleAspGlySerAspHisSerVa 774 |:::|||::::: GGAGGTGTTAAATCACTCTGACCATCACCC 2449 VValTyrThrPheHisLeuArgValThrAs 794 SATCTCTTTGCCAACCACTTCTACAGTCAT 1489 |||| | ||||:: |||||| :: reggaatgtegttaccctacccaceae 2329 PAGCCAGAGCCCCGTAAGAATCGGCCCCC 1429 LeuThrieuProleuThrSerAlaLeuIl 454 SerLeuGlyProGlySerGluGlyLysHi 574 vGlyArgHisValLeuValLeuProAsnAs 734

for suppressing cancer cell growth.

ONCOLOGY

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Claim 5; SEQ ID NO 7; 45pp; Chinese.
                              08-FEB-2001; 2001CN-00105311,
               08-FEB-2001; 2001CN-00105311
                                             (SHAN-) SHANGHAI INST
                                                                                                   Human protein useful
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    A---AATCACCTCTGGCTTCTTGAAGGAACCCCTCTCTCCAGTCATGTTGGGCTGCTG
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The invention relates to a novel human protein with cancer inhibiting function. Also disclosed is the polynucleotide encoding the protein, a method for preparing the polypeptide by a recombinant technique, and an antagonist against the polypeptide by a recombinant technique, and an treating diseases, such as cancers. The polypeptide is useful for treating diseases, such as cancers. The current sequence represents a human cancer inhibiting protein encoding CDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aArglysGlnCysSerGluGlyArgThrTyrSerAsnAlaValIleSerProAsnLeuGl
                                                                                                                                                                                                       Other;
                                                                                                                                                                                                    Sequence 4001 BP; 1057 A; 1044 C; 1037 G; 863 T; 0 U; 0
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                    Length:
Matches:
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                                                                                                                                                                                                                             3108 AGTACAAGATCCTGGATGCCACGGAT---CAGGAAAGCCTGGAGCTGAAGCCTCCC 3164
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                                                                                                     954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, bone marrow, antiinflammatory, cytostatic, neuroprotective, antiviral, antibacterial, antifungal, anti-HIV; haemostatic; immunosuppressive; gene therapy, cytokine cell proliferation; cell differentiation modulator; immune disorder; infection, cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.
                                                                   2871 AGCTGAACTGTTCCGACCATGGCCACTGTGACTCGTTCACCAACGCTGTATCTGTGACC
 erLysGluLysAlaAspPheLeuLeuPheLysValLeuArgValAspThrAlaGlyCysL
             914 euleulysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCysIleCysSerH
                                                                                                     934 isLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSerAsnCysGluT
                                                                                                                                                                       hrTrpLeuCysIleCysCysLysArgGlnLysArgThrLysIleArgLysLysThrL
                                                                                                                               CTTTTTGGATGGAGATTTTCATCAAGGTGCAGCTGAGGGATGGAGACAGCAACTGTGAGT
                                                                                                                                                        rpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLeuThrGlyGlyPheT
                                                                                                                                                                                                                                                             ysTyrThr11eLeuAspAsnMetAspGluGluGluArgMetGluLeuArgPro----L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human bone marrow cDNA, SEQ ID NO: 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-00488725.
2000US-00552117.
2000US-0059042.
2000US-00653450.
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2000US-00653450.
2000US-00653450.
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25-APR-2000;
20-JUN-2000;
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03-AUG-2000;
14-SEP-2000;
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130 TrpGlyAspSerProGluAspIleArgLysAspLeu***PheLeuGlyLysAspTrpGly 149
                                                                                                                                                                                                                The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accerrererecirierea Academee 2395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 ACACAATTTGGAGTTGGCCTGAGATCTGGGGGAGAA---AATCACCTCTGGCTTCTTGAA 452
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                                                                                                                               Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders.
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Δ Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3918 BP; 1017 A; 1023 C; 1013 G; 865 T; 0 U; 0 Other,
     3J, Tang YT, Liu C, Asundi V, Chen R, M
Werhman T, Xu C, Xue AJ, Yang Y, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3918
516
134
316
131
                                                                                                                                                                                                                                                                                                                                                                                                                                            screening of chemical compounds as potential drugs
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Matches:
Conservative:
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                                                                                                                                                                                      English
       Boyle BJ, Tang YT,
                                                                                                                                                                                      Claim 1; Page 228-229; 648pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.56e-129
2293.50
59.25$
47.04$
                                           Drmanac RT;
                                                                             WPI; 2001-488707/53.
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Best Local Similarity:
                                                                                                 P-PSDB; AAM00789
                          Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                        Ren F, W
Zhou P,
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190 GitySerGluGityAlaPheAsnSerSerValGityAepSerProAlaValProAlaCurth 130 GitySerGluGityAlaPheAsnSerSerValGityAepSerProAlaValProAlaProLyAEa 131 GittGlinAspProGluEuwHisTyTeuwBrGluSerAlaSerThrProAlaProLyAEa 132	20	22		933 Qy 582 ThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAl 265			307 Gy 642 1073 Db 2070		1133 Qy 681 1ThrGlyLeuGlnValGlyThrTyrHiePheArgLeu' 1342			741 rArgserThrAspAspGlnArglleValSerTyrLeu' (402		442 CY 781 442 Db 2490 1469		481	158 501	: 1649 Qy 861 erAspLeuSerThrVallleValPheTyrValGlnSe: : 521
	er	GInGinAspProGluLeuHisTyrLeuAsnGluSerAlaS	756 CAGCAGSerValLeuLeuProLeuProThrThrProSerGly 230 ProGluArgSerValLeuLeuProLeuProThrThrProSerSerGly	780 CAGAAGAGAGGTAGTCCCAGTGACGTAGTTACACCTATAGTGACACACAGCATTCT 246 GluValLeuGluLysGluLysAlaSerGlnLeuGlnGluGlnSerSerAsnSerSerGly ::: ::: 834 AAAGTGAATGACTCCAACGAATTAGGTGGTCCTACACTACCAGTGGTCTACAGAGTCAA	266 LysGluValLeuMetProSerHisSerLeuProProAlaSerLeuGluLeuSer 804 AAGGGGATTAATAAATTTTCAGTCCCCTAAACAACAGAACAGAAGAAGAAGAAGAAGAAGAAGAAGAA	284SerValThrValGluLysSerProValLeuThrValThrProGlySer 	300ThrGluHisSer11eProThrPro	308ProThrSerAlaAlaProSerGluSerThrProSerGluLeuPro	10/4 IACAGIIAIGCIACCCCIACCCCCCAGGCCICIIICCAGAGCACCICAGGACCCAGAGCCCAGGAGCAGCCAGGAGCACCCAGGAGCAGC	343 LeulleileThrLeuProAspAsnGluValGluLeuLysAlaPhe-ValAlaProAla-P 1170 GHCCAAAHAAACCCCCAAACCAAACAAACAAAAAAAAAA	362 roProValGluThrTyrAsnTyrGluTrpAsnLeuIleSerHisProThrAspTyrG	1250 CACCIMANGGAGAMACCIACGACIGGACIGALIACICAICAGAGACATACA 382 InGlyGlulleLysGlnGlyHisLysGlnThrLeuAsnLeuSerGlnLeuSerValGlyL 1200 CHCGACAAAATGCAAAAAAACCAAAAAAAAAAAAAAAAAA	402 euTyrValPheLygValThrValSerSerGluAsnAlaPheGlyGluGlyPheValAsnValOntricent Constructions of the control of the	422 alThrVally8ProAlaArgArgValAsnLeuProProValAlaValValSerProGlnL	442 euGlnGluLeuThrLeuDroLeuThrSerAlaLeulleAspGlySerGlnSerThrAspA	462 spThrGluile-ValSerTyrHisTrpGluGluileAsnGlyProPheileGluGluiye	1530 ATGATAAATCCGTTCAGTACCATTGGGAAGAACTTAAGGGGCTCTCTAAGAAGAAAAAAAA	1590 ATTTCTGAAGATACAGCCATATTAAAACTAAGTAAACTCGCCCCTGGGAACTACACTTTC 502 ArgleuThrValThrAspSerAspGlyAlaThrAsnSerThrThrAlaAlaLeuIleVal

UThrVallysAspGlnGlnGlyLe 701 ABPTYTThrPheGlnLeuLysval 601 indenSerileThrLeudapGlySe 741
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GAGCACATCAGAGCTGGATGGCTC 2369 hraspSerGlnGlyalaSerAspT 801 rgiysserglyLeuValGluLeuT 821 ||||||:: |||||||:: |GGAAAACAACCTGGTGGAGATCA 2609 rgLysAspThrLeuValArgGlnL 841 acgagccrcccaccagarctra 2789 GlyProAsnHisThrIleThrLeu 541 SGIULEUIIEPheProValGluSer 641 ||||||| |GAGCTGACCCTTCCTGTGGATAGC 2069 GGIYIlevalPheTyrHisTrpGlu 661 ### BEST | 121 | 121 | 122 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 123 | 1 ysvalglnLyslleArgAlaHisS 861 erArgProProPheLysValLeuL 881 HisyalvalMetGlnGlyvalGln 581 urrplleArg-AspGlyGlnSerP 761 tArgLeuSerLysGluLysAlaAspPheL 901

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SerGlyLysGlnGluProArgGlySerAlaGluTyrThrAspTrpGlyLeuLeuProGly 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerThrProAlaProLysLeuProGluArgSerValLeuLeuProLeuProThrThrPro 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 SerSerGlyGluVal---LeuGlu------LysGluLysAlaSerGlnLeuGlnGlu 258
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2278.00
63.16%
50.99%
40.82%
 03-MAY-2002; 2002US-0377883P
                                                                                                                                                         WPI; 2003-845310/78.
                                           (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                  e.g. neuromuscular, and/or infections.
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Best Local Similarity:
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2790 AAGGCCATGAGGTGGCATGCTCAAGAGTGAGCTGCGGAAGCAAAAGGCAGACTTT
                                                           2850 TGATATTCAAAGCCTTGGAAGTCAACACTGTCACATGTCAGCTGAACTGTTCCGACCATG
                                                                                                921 lyHisCysAspProLeuThrLysArgCysIleCysSerHisLeuTrpMetGluAsnLeuI
                                                                                                                                                                                                                                    3030 CAGAGTGGAGCGTGGTTATATGTTATCATTGCTACCTTTGTCATTGTTGTTGTTGCTTGGGA
                                                                                                                                                                                                                                                                                                                                                    euLeuPheLysValleuArgValAspThrAlaGlyCysLeuLeuLysCysSerGlyHisG
                                                                                                                           941 leGlnArgTyrIleTrpAspGlyGluSerAsnCys-------
                                                                                                                                                                                                                   953 --GluTrpSerIle-PheTyrValThrValLeuAlaPheThrLeuIleValLeuThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                     3204 ACCTCCCGAGCAGGCATCAAACAGAAAGGCCTTTTGCTAAGTAGCAGCCTGATGCACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECP; secreted protein; neuroprotective; relaxant; antithyroid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1050 AsnProLysValSerMetAsnGlySerIleArgAsnGly 1062
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204

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37

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3628 490 1117 253 102

Length: Matches: Conservative: Mismatches:

Indel8: Gaps:

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the invention trainers to a novel isolated safe, becated protein)

polypeptide. The polypeptide of the invention demonstrates

cermatological, immunosuppressive, antidiabetic, cytostatic,

dermatological, immunosuppressive, antidiabetic, cytostatic,

antiallargic, cerebroprotective, gastrointestinal, hepatotropic,

antiparasitic, anticonvulsant, antiparkinsonian, antibacterial,

cereivities. The polypeptide may be useful in diagnosing, preventing and

certivities. The polypeptide may be useful in diagnosing, preventing and

treating disorders including neurodegenerative disorders such as

continhematic, cardiant, cardiants, anti-HIV and nootropic

activities. The polypeptide may be useful in diagnosing, preventing and

treating disorders including neurodegenerative disorders including

controlic dystrophy and catatonia, endocrine disorders particularly

controlic dystrophy and catatonia, endocrine disorders particularly

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controlic dystrophy and catatonia, endocrine disorders

controlic dystrophy and alsease, ranal disorders e.g. Goodpasture's

controlic diseases particularly viral, bacterial, fungal, parasitic,

cond hepatic diseases particularly viral, animals, as well during gene

controlic dystrophy procedures. The current sequence is that of the human SECP cDNA
                                                                                                                                                                                                                                                                      Marquis JP, Lee SY, Elliott VS, Ramkumar J, Hafalia AJA;
Kable AB, Chawla NK, Emerling BM, Khare R, Jiang X, Jackson AA;
Hawkins PR, Jin P, Mason PM, Richardson TW, Swarnakar A, Lal PG;
Warren BA, Lee S, Griffin JA, Pu GK, Wilson AD, Xu Y, Bulloch SA;
Becha SD, Bhatia UG, Burrill JD, Blake JJ, Ho A, Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New SECP polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of SECP, e.g. neuromuscular, immunological, cardiovascular disorders, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to a novel isolated SECP (secreted protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 84; 300pp; English.
24-MAY-2002; 2002US-0383218P
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1234 AACTCCATCACCTTTTGGGAACCAGAGCACTGATGATCATGGCATCACCAGCTATGAG 1293 564 TTpSerLeuGlyProGlySerGluGlyLy8Hi8ValValMetGlnGlyValGlnThrPro 583 [1354 ACCTTÁCAGCTCTGCGÁTGCAÁGÁGÁGACACTÁCACTTACCÁGCTCACAGTGÁCTGÁC 1413 604 SerSerÁrgGInGInSerThrala***ValThrVallIleValGInProGluAsnAsnArg 623 ::: :::		LeuaspGlyserSerSerSeraspaspHisGlylleValPheTyrHisTrpGluHisVal 	664 ArgGlyProSerAlaValGluMetGluAsnileAspLysAlaileAlaThrValThrCly 683 :::	684 LeuGlnValGlyThrTyrHisPheArgLeuThrValLysAspGlnGlnGlyLeuSerSer 703 	704 ThrSerThrLeuThrValhlaValLysEJuAsnAsnSerProProArgAlaArgAla 723 :::::	724 GlyGlyArgHisValLeuValLeuProAsnAsnSerIleThrLeuAspGlySerArgSer 743	744 ThraspaspGlnArgileValSerTyrLeuTrpIleArgAspGlyGlnSerProAlaala 763 :::	764 GlyaspvallleaspGlySeraspHisSerValAlaLeuGlnLeuThrAsnLeuValGlu 783 ::: :::				844 LeuLeuAsnValLeuAspSerAspIleLysValGlnLysIleArgAlaHisSerAspLeu 863 	864 SerThrVallleValPheTyrValGlnSerArgProProPheLysValLeuLysAlaAla 883	884 GluvalalaArgAsnLeuHisMetArgLeuSerLysGluLysAlaAspPheLeuLeuPhe 903 	904 LysValLeuargValAspThralaGlyCysLeuLeuLysCysSerGlyHisGlyHisCys 923 :::
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GTCAAGCCAATCC 238 258 TGGTTGAGAAGCCT 298		GGIGGCCA 417. SGIYSer 299 ::: SAGCACTCAA 477			snLeu :::::	ro Pro	1ng1y	eufyr 	alThr							
CTGGGAGTCAA	TTGTCAACAGG	hrValThrPro	thrPro pagccagtggct	hrProSerGlu :::	AlSerAlaGly	hevalAlaPro	iisProThrAst	Sintenserval	luglyPheval	AlvalSerPro	serginserthr GTCAAAGCACT	PhelleGluGlu TAAGAGAAGAC	31 yAsnTyrSer	AlaAlaLeuIle	isThrileThi	isGlnIleval
TGTACTGGTTCTGCCTGTCTGGAGGGCCATGGAGAGAGGCTGGGAGTCAAGCCA TGTACTGGTTCTGCCTGTCTGGAGGGCCATGGAGAGAGAG	GTACCTGTTTTATACTTTGCTTCAGCGTTCTGTGGTTGTCAACAGGTCCAGLUValLeuWet ProSerHisSerLeuProProAlaSerLeuGluLeuSer	GUGATIALAATITICCAGICCCUTAACCACAGACTIGACTIGAGGGTGTGTCTGGTGTGTGTGTGTGTGTGTGTGTGTGTG			SerProThrThrAlaProArgThrValLysGluLeuThrValSerAlaGlyAspAsnLeu ::: ::::::	IlelleThrLeuProAspAsnGluValGluLeuLysAlaPheValAlaProAlaP 	ValGluThrThrTyrAenTyrGluTrpAenLeulleSerHisProThrAepTyrGluGly	Garage G	404 ValPheLysValThrValSerSerGluAsnalaPheGlyGluGlyPheValAsnV 	VallysProhlaArgArgValAsnLeuProProValAlaValValSerProGlnLeuGln	GluLeuThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThrAspAspThr ::::::		ValAspSerProValLeuArgLeuSerAsnLeuAspProGlyAsnTyrSerPheArgLeu	GRAGGALACCAGCCAIAITARACLAGGATACCCIGGGAACTACACTICAGGIIG ThrValThrAspSerAspGlyAlaThrAsnSerThrThrAlaAlaLeuIleValAsnAsn 	AlaValAspTyrProProValAlaAsnAlaGlyProAsnHisThrIleThrLeuProGln	AsnSerileThrLeudsnGlyAsnGlnSerSerAspAspHisGlnIleValLeuTyrGlu
 rcTGGAGGCC SAGATATTATT	CTTTTGCTTC	CCCCTAACCA(ValGluLy8Se	ThrGluH	SerAlaAlaPı 	ArgThrValLy:::	AsnGluValG]	TyrGluTrpAt	SLYSGINThrie	SerSerGluAr	yalAsnLeuP	Thrseralate	strpGluGluI.	ArgleuserA	oglyalaThrai GGAGCTACCA	ovalAlaAsnA	161 VASHG1 HS
GTTCTGCCTG1	TTTTATACTTC	SerValThi TATCAGTGCAJ	AAAGTTCTGAG	ProTh:	hrThrAlaPro	hrLeuProAsi	hrThrTyrAsr	ysglnglyHie	ysvalThrval	roalaargard	hrLeuProLet :: :crTrGCCAAC(alSerTyrHis	erProValle	hraspserasi	SpTyrProPro	Terrecedes:
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AspProLeuThrLysArgCysIleCysSerHisLeuTrpMetGluAsnLeuIleGlnArg
                                                             SerArgGluLysMetGluArgGlyAsnProLysValSerMetAsnGlySerIleArgAsn
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                       944 TyrileTrpAspGlyGluSerAsnCysGluTrpSerilePheTyrValThrValLeuAla
                                                                                               PheThrLeulleValLeuThrGlyGlyPheThrTrpLeuCyslleCysCysCysLysArg
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                                                                                                                                                                                                GingluargMetGluLeuArgPro----LysTyrGlyIleLysHisArgSerThrGlu
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T;
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, Otsuki
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A, Nagai K,
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Sugiyama T, Wakamatsu
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27-AUG-1999; 99JP-00300253.
Il-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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the present invention describes primer sets for synthesising 5002 full-complementary defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonuclectide complementary to the complementary strand of a polymuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the chigonucleotide comprises at least 15 nucleotides; or (b) a combination of a polymucleotide which comprises a 5'-end complementary strand of a polymucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a complementary strand of a polymucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the complementary to a coligonucleotide comprises a 1'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in geneticularly full-length cDNAs. The primers are also useful for the categorical and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and sequences; AAH13613 to AAH1842 represent human amino acid sequences; and AAH13629 to AAH13622 represent colligonucleotides. all of which are used in the exemplification of the primer sets for synthesising 5602 fullpresent invention

Sequence 2796 BP; 763 A; 732 C; 711 G; 590 T; 0 U; 0 Other;

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542
                                                                                                  LeuLysAlaPheValAlaProAlaProProValGluThrThrTyrAsnTyrGluTrpAsn 373
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GlyProAsnHisThrIleThrLeuProGlnAsnSerIleThrLeuAsnGlyAsnGlnSer 553

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8; SEQ ID NO 18736; 2537pp + Sequence Listing; English

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                                                                                                               934 HisLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSerAsnCysGlu 953
                                                                                                                                                                                                   TrpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLeuThrGlyGlyPhe 973
                        LeuLeuLysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCysIleCysSer
                                                                                                                                         CCTTTTTGGATGAGAATTTCATCAAGGTGCAGCTGAGGGATGGAGACAGCAACTGTGAG
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                                                                      AspTyrThrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThrAla***Val
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This full-length cDNA clone, designated cw1233 3, codes for a novel human secreted protein (see AAW69430), i.e. cw1233 3 protein. It was isolated from a human foetal brain cDNA library using methods which are selective from a human foetal brain cDNA library using methods which are selective cor cDNAs encoding secreted proteins, or was identified as encoding a secreted protein on the basis of computer analysis of the encoding protein. Homology is shown to some database sequences. The invention provides isolated polymucleotides (see AAV58754-63) obtained from human adult testis, brain, retina or placenta, or from foetal kidney or brain cDNA libraries. These are all deposited as ATCC 98353. They canced novel human secreted proteins (see AAW65423-33) that may have e.g. nutritional activity, immune stimulating or suppressing activity, haemostatic activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, antiinflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition or other activities. They may also be used for diagnostic purposes

Sequence 2501 BP;

361 GAGATGCAGGTGTTAGAACACCAACCTTACAGCTCTCTGCGATGCAAGAAGAGAACACAAC IlevalGlnProGluAsnAsnArgProProValAlaValAlaGlyProAspLysGluLeu ProPhelleGluGluLysThrSerValAspSerProValLeuArgLeuSerAsnLeuAsp ProGlyAsnTyrSerPheArgLeuThrValThrAspSerAspGlyAlaThrAsnSerThr ACTGCAAACCTGACAGTGAACAAAGCTGTGGATTACCCCCCTGTGGCCAACGCAGGCCCC ValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMetGlnGluGlyAspTyr GlySerGlnSerThrAspAspThrGluIleValSerTyrHisTrpGluGluIleAsnGly CCTGGGAACTACACTTTCAGCTTGACTGTAGTAGACTCTGATGGAGCTACCAACTCTACT ThralaalaLeuIleValAsnAsnAlaValAspTyrProProValAlaAsnAlaGlyPro AspHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySerGluGlyLysHisVal ThrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThrAla***ValThrVal Conservative: Mismatches: Indels: Gaps: Length: Matches: US-10-764-390-3 (1-1072) x AAV58761 (1-2501) 1.06e-100 1817.50 73.23% 60.10% 32.57% :: Local Similarity: Percent Similarity: Best Local Similari Alignment Scores: 476 241 596 421 919 481 216 181 536 556 301 456 19 496 121 Query Match: DB: a a 셤 & 8 ò 임 δ ò ઠ 요 ઠે g ò ያ ያ 8 S

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ceacargaegeaecccaecaccaccaceaecrerraaarcacrercaccarcacccrarc 959 1014 GlyllelysHisArgSerThrGluHisAsnSerSerLeuMetValSerGluSerGluPhe LeuGlnLeuThrAsnLeuValGluGlyValTyrThrPheHisLeuArgValThrAspSer GlyLeuValGluLeuThrLeuGlnValGlyValGlyGlnLeuThrGluGlnArgLysAsp LysileArgAlaHisSerAspLeuSerThrValIleValPheTyrValGlnSerArgPro GIGTTATATGITATCATTGCTACCTTTGTCATTGTTGTTGTTGCTTGGGAATCCTGTCTTGG ThrileieuAspAsnMetAspGluGluGluArgMetGluLeuArgPro-----LysTyr GlnGlyAlaSerAspThrAspThrAlaThrValGluValGlnProAspProArgLysSer LysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCysIleCysSerHisLeu IlePheTyrValThrValLeuAlaPheThrLeuIleValLeuThrGlyGlyPheThrTrp LeuCyslleCysCysLysArgGlnLysArgThrLysIleArgLysLysTyr 736 IleThrLeuAspGlySerArgSerThrAspAspGlnArgIleValSerTyrLeuTrpIle ArgAspGlyGlnSerProAlaalaGlyAspValIleAspGlySerAspHisSerValAla ThrLeuValArgGlnLeuAlaValLeuLeuAsnValLeuAspSerAspIleLysValGln ProPhelysValleuLysAlaAlaGluValAlaArgAsnLeuHisMetArgLeuSerLys AGCAGTGTTGCTACTGTGACTGGGCTGCAAGTGGGGACCTATGTGTTCACCTTGACTGTC LysAspGlnGlnGlyLeuSerSerThrSerThrLeuThrValAlaValLysGluAsn AsnSerProProArgAlaArgAlaGlyGlyArgHisValLeuValLeuProAsnAsnSer AACAAACCACCTATAGCCAAGATAACTGGGAATGTGGTGATTACCCTACCCACGAGCACA LyBAlaIleAlaThrValThrGlyLeuGlnValGlyThrTyrHisPheArgLeuThrVal <u>:</u> 964 918 1140 1200 1260 1320 1380 1500 916 900 960 856 876 896 926 716 780 840 836 721 756 176 919 969 දු ද 요 ઠે 유 셤 ઠે g ð g ઠે g ઠે 8 S 음 장 g ò 셤 8 셤 ð 셤 ⋩ 셤 ò 셤 8 & ద ઠે 8 ठ 540 675 480 635 655 600 9 180 240 420 615 9 ATTGTGCAACCTGAAAACAATAAGCCTCCTCAGGCAGATGCAGGCCCAGATAAAGAGCTG IlePheProValGluSerAlaThrLeuAspGlySerSerSerSerAspAspHisGlyIle ValPheTyrHisTrpGluHisValArgGlyProSerAlaValGluMetGluAsnIleAsp ACCCTTCCTGTGGATAGCACAACCCTGGATGGCAGCAAGAAGCTCAGATGATCAGAAAATT 646 G; 523 T; 0 U; 1 Other; 682 A; 649 C;

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Search completed: October 12, 2005, 10:55:37 Job time: 1339 secs

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; Bublication No. US20050196754A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790C1P3/US
; CURRENT PAPLICATION NUMBER: US/10/450,763
; CURRENT PLINUG DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR PILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-03-31
; RIOR FILING DATE: 2000-03-31
; ROR PRILICATION NUMBER: 09/649,167
; ROR APPLICATION NUMBER: 09/649,167
; RORD APPLICATION NUMBER: 2000-03-33
; SOFTWARE: CLUSCONO-03-33
; ELENGTH: 19
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1.7%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels
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NAME/KEY: misc_feature
LOCATION: (1) ... (19)
COTATION: (3) ... (19)
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US-10-764-390-51

US-10-764-390-53

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US-10-764-390-65

US-10-764-390-60

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Sequence 43, Appl
Sequence 265, App
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-764-390-43
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US-10-764-390-268
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                                                                                                                                                               October 12, 2005, 10:22:50
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                                                      Sequence 43, Application US/10764390

Sequence 43, Application US/10764390

Belication No. US20040214212A1

GENERAL INFORMATION:

APPLICANT: Ratiano, Arthur B.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Ge, Wangmaco

APPLICANT: Faris, Mary

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APPLICANT: Faris, Mary

APPLICANT: Faris, Mary

APPLICANT: Faris, Mary

TITLE OF INVENTION: Nordeic Acids and Corresponding Proteins

TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of

TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of

TITLE OF INVENTION WUMBER: US/10/764,390

CURRENT FILING DATE: 2004-01-23

PRIOR FILING DATE: 2004-01-23

PRIOR FILING DATE: 2003-01-24

NUMBER OF SEQ ID NOS: 277

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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Baitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION CANCER: 2004-01-23
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE PARESEQ for Windows Version 4.0
SEQ ID NO 265
LENGTH: 24
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1.5%; Score 16; DB 16; L
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
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Publication No. US20040214212A1
GENERAL INFORMATION;
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Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-764-390-265
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; ORGANISM: Homo sapiens
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US-10-764-390-265
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0.8%; Score 9;
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Sequence 46, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
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Publication No. US20040214212A1
GENERAL INFORMATION:
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                                                                                                                   Query Match 0.8
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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    ; ORGANISM: Homo sapiens
US-10-764-390-45
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US-10-764-390-46
                                                                                                                                                                                                                                                                                                                    1 GVLSSLLLL 9
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APPLICANT: Agensys, Inc.
APPLICANT: Agensys, Inc.
APPLICANT: Jacobovits, Aya
APPLICANT: Jacobovits, Aya
APPLICANT: Jacobovits, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Ge, Wangmao
APPLICANT: Juan J. Perez-villar
APPLICANT: Juan J. Perez-villar
APPLICANT: Juan J. Perez-villar
APPLICANT: Juan J. Perez-villar
APPLICANT: Juan J. Perez-villar
APPLICANT: Silsa-20081:00
TITLE OF INVENTION: Entitled 254PID6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
TITLE OF INVENTION UNMERR: US/10/764,390
CURRENT APPLICATION NUMBER: US/0/442,526
FRIOR PEDICATION NUMBER: US/0/442,526
FRIOR PEDICATION WINGER: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 9
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APPLICANT: Raitano, Arthur B.
APPLICANT: Saitano, Arthur B.
APPLICANT: Challite-Eid, Pia M.
APPLICANT: Challite-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-villar
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
FRIOR PELION NUMBER: US60/442,526
FRIOR FILING DATE: 203-01-24
NUMBER OF SEQ ID NOS: 277
SOOFWARE: FastSEQ for Windows Version 4.0
SUPPLY: RAILING DATE: PARTER ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACIDS ACID
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0.8%; Score 9; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
Query Match
1.3%; Score 14; DB 16; L
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 14; Conservative 0; Mismatches 0;
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; Sequence 44, Application US/10764390
; Publication No. US20040214212A1
; GENERAL INFORMATION:
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; Publication No. US20040214212A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-764-390-44
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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US(0/442,526
PRIOR APPLICATION NUMBER: US(0/442,526
NUMBER OF SEQ ID NOS: 277
SOFTWARE: Fast-SEQ for Windows Version 4.0
SOFTWARE: Fast-SEQ for Windows Version 4.0
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Takabovits, Aya
APPLICANT: Jakbovits, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
CURRENT FILING DATE: 2004-01-23
FRIOR APPLICATION NUMBER: US60/442,526
FRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
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0.8%; Score 9; DB 16; Length 9; 100.0%; Pred. No. 1.7e+06; tive 0; Mismatches 0; Indel8
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RESULT 13
US-10-764-390-51
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j Sequence 49, Application US/10764390

j Sequence 49, Application US/10764390

j Publication No. US20040214212A1

GENERAL INFORMATION:

j APPLICANT: Raitano, Arthur B.

j APPLICANT: Baitano, Arthur B.

j APPLICANT: Ge, Wangmao

j APPLICANT: Farish, Mary

APPLICANT: Farish, Mary

j APPLICANT: Farish, Mary

j APPLICANT: Farish, Mary

j APPLICANT: Steven B. Kanner

j APPLICANT: Braitsh Mary

j APPLICANT: Steven B. Kanner

j TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of

j TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of

j TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of

j CURRENT APPLICATION NUMBER: US60/442,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Taitano, Arthur B.
APPLICANT: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Janny: Ja
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Best Local Similarity 100.
Matches 9; Conservative
                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-10-764-390-47
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SEQ ID NO 47
                                         LENGTH: 9
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Sequence 51, Application US/10764390

Publication No. US20040214212A1

GENERAL INFORMATION:

APPLICANT: Raitano, Arthur B.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Greven B. Kanner

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Kanner

APPLICANT: Steven B. Tanner

TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

FILE REFERENCE: 51158-20081.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Bandovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Brish Mary
APPLICANT: Brish Mary
APPLICANT: Brish Mary
APPLICANT: Brish Mary
APPLICANT: Brish Marie Acids and Corresponding Proteins
TITLE OF INVENTION: Butitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Brish Mark Willing DATE: 2004-01-23
FILE REFERENCE: 2004-01-23
FRIOR APPLICATION NUMBER: US60/442,526
FRICH APPLICATION NUMBER: US60/442,526
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
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0.8%; Score 9; DB 16; Le
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENCTH: 9
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 50, Application US/10764390; Publication No. US20040214212A1; GENERAL INFORMATION;
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US-10-764-390-50
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US-10-764-390-49
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US-10-764-390-52
; Sequence 5.2, Application US/10764390
; Publication No. US20040214212A1
GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: GENERAL B. Kanner
; APPLICANT: Steven B. Kanner
; APPLICANT: Steven B. Kanner
; APPLICANT: Steven B. Kanner
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; TITLE OF INVENTION: Cancer
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20081.00
; CURRENT PILING DATE: 2004-01-23
; PRIOR FILING DATE: 2004-01-23
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 277
; SEQ ID NO 52
; LENGTH: 9
; TVDD: NOS:
; TVDD: NOS:
; SEQ ID NO 52
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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
                                                                                                                                                                                                                                                          0.8%; Score 9; DB 16; Length 9; 100.0%; Pred. No. 1.70+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     0; Indels
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0.8%; Score 9; DB 16; Le
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US60/442,526
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SEQ ID NO 51
LENGTH: 9
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                                                                                                                                                                                                                                                          Query Match 0.8
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-390-52
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                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-390-51
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TITLE OF INVENTION: Entitled 254PlD6B. Useful in Treatment and Detection of
FILE OF INVENTION: Cancer
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
FRIOR PRILING DATE: 2004-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-764-390-53
Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.76+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
OP
Search completed: October 12, 2005, 10:27:51
JOB time: 70 secs
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
  US-08-666-473-53
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8, Appli
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Appl
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Sequence 8, Ap
Sequence 8, Ap
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Sequence 78,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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Sequence 1
Sequence 2
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(Ggn2_6/ptodata/1/iaa/5A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/5B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*);
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-36-347F-78

US-09-873-637-14

US-09-873-637-14

US-09-873-637-14

US-09-042-353-320

US-09-042-353-320

US-09-0417A-168

US-09-0417A-168

US-09-178-8

US-08-537-811A-41

US-08-537-811A-45

US-08-537-814A-50

US-08-248-899C-53

US-08-347-198A-11

US-08-347-198A-11

US-08-347-358-185

US-09-129-366-50

US-08-877-7598-185

US-08-877-7598-185

US-08-877-7598-185

US-08-877-7598-185

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US-09-889-136-6
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                                                                                                             protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Match Length
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APPLICANT: YOSHIDA, Aruto
APPLICANT: YOSHIDA, Aruto
APPLICANT: TAKEUCHI, MAKOCO
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEB: FOLEY & Lardher
STREET: 3000 K Street, N.W., Suite 500
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CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
FILING DATE: 19-SEP-1996
CLASSIFICATION ADATA:
APPLICATION NUMBER: WO PCT/JP95/02238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-22101
FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-269111
FILING DATE: 01-NOV-1994
ATONEY/AGENT INPORMATION:
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
RELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
                                                       US-08-232-513A-15
US-08-441-594A-6
US-09-211-159-4
US-08-611-307-4
US-08-611-307-4
US-08-611-307-4
US-09-128-721-14
US-09-128-722-14
US-09-128-722-14
US-09-128-722-14
US-09-128-71-190
US-09-467-023-232
US-09-47-023-232
US-09-411-10
US-09-346-88A-13
US-09-348-578-4
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US-09-348-578-4
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US-09-348-578-4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-261-855-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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US-08-096-762-205
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US-09-873-637-14
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                     US-09-261-855-14
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Sequence 78 Application US/09001984C

Sequence 78 Application US/09001984C

Patent No 624531;
GENERAL INFORMATION:
APPLICANT: Laal, Suman
APPLICANT: Laal, Suman
APPLICANT: Belisle, John T

TITLE OF INVENTION: BARLY DETECTION OF WYCOBACTERIAL DISEASE
FILE REFERENCE: NYU-011
CURRENT APPLICATION NUMBER: US/09/001,984C
CURRENT FILING DATE: 1997-12-31
PRIOR APPLICATION NUMBER: 60/034,003

PRIOR PLING DATE: 1996-12-31
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
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Fatent No. 6506384
GENERAL INFORMATION:
APPLICANT: Laal, Suman
APPLICANT: Laal, Suman
TITLE OF INVENTION: EARLY DETECTION OF WYCOBACTERIAL DISEASE
TITLE OF INVENTION: EARLY DETECTION OF WYCOBACTERIAL DISEASE
CURRENT APPLICATION NUMBER: US/09/396,347F
CURRENT FILING DATE: 1999-09-14
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR APPLICATION NUMBER: 09/001,984
PRIOR APPLICATION NUMBER: 09/001,984
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2.1
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                                      0.6%; Score 6; DB 2; Length 7;
100.0%; Pred. No. 4.1e+05;
iive 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 10
; TYPE: PRT
ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-396-347F-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-78
                                    Query Match 0.6
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                         222 ASTPAP 227
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US-09-396-347F-78
US-08-666-473-53
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LENGTH: 10
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3 APAPPV 8

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Sequence 14, Application Us/09561855A

Sequence 17 Title OF INVENTION: THE CAP CODING REGION DETERMINANT-BINING PROTEIN
TITLE OF INVENTION: THE CAP CODING REGION DETERMINANT-BINING PROTEIN
TITLE OF INVENTION: THE CAP CODING SEGUENCE
TITLE OF INVENTION: CREATER CAP CODING SEGUENCE
TITLE OF INVENTION: CREATER CAP CODING SEGUENCE
TITLE OF INVENTION: CREATER CAP CODING SEGUENCE
TOWARTH FILING NAME: 1999-01-03
SOURSEL FROM SEGUENCE SEGUENCE
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us-10-764-390-3.011.rai

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TYPE: amino acid
STRANDEDNESS:
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Factor No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ADDRESSEE FRANCISCO
STATE: California
COUNTRY: USA
ADDRESSEE FORM:
AMBIUM TYPE: Floppy disk
AMBIUM TYPE: Floppy disk
AMBIUM TYPE: Floppy disk
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION NUMBER: US 08/053,131
PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 26-APR-1993
PRIOR APPLICATION NUMBER: US 07/990,668
FILING DATE: 3-JUN-1992
PRIOR APPLICATION NUMBER: US 07/904,068
FILING DATE: 33-JUN-1992
PRIOR APPLICATION NUMBER: US 07/813,408
FILING DATE: 33-JUN-1992
PRIOR APPLICATION NUMBER: US 07/813,408
FILING DATE: 33-JUN-1992
PRIOR APPLICATION NUMBER: 30,223
PRIOR APPLICATION NUMBER: 30,223
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELEPHONE: 415-326-2420
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LINFORMATION POR END IND ACIDS
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 VTVSSE 412
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US-09-042-353-320
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Gaps
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0.6%; Score 6; DB 3; Lei
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-042-353-320
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7 VTVSSE 12

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10 SLLLLV 15
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                          US-09-044-718-8
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                                         Sequence 168, Application US/08758417A
Patent No. 6300129
GENERAL INPORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compartible
COMPUTER: TBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-0CT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-0CT-1995
APPLICATION NUMBER: US 08/32,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MRX-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 12-DEC-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/095,762
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/095,762
FILING DATE: 16-DEC-1993
APPLICATION NUMBER: US 08/095,762
FILING DATE: 16-DEC-1992
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 168:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 417
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
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RESULT 8
US-08-758-417A-168
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100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 15;
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100.0%; Pred. No. 2.5
tive 0; Mismatches
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Sequence 8, Application US/10062848

Sequence 8, Application US/10062848

Sequence 8, Application US/10062848

GENERAL INCEMATION:
APPLICANT: ROSTREWA, Dirk
APPLICANT: TOMCSH, Andrea
APPLICANT: TOWCSH, Aurt
APPLICANT: VORSH, Kurt
APPLICANT: WOSS, Markus
APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/044,718
PRIOR APPLICATION NUMBER: 09/044,718
PRIOR APPLICATION NUMBER: EP 97810175.6

PRIOR APPLICATION NUMBER: EP 97810175.6

PRIOR FILING DATE: 1997-03-25

NUMBER OF SEQ ID NOS: 82

SEQ ID NO 8

SEQ ID NO 8
                                                                     APPLICANT: KOSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: TOMSCHY, Andrea
APPLICANT: VAN LOON, Adolphus
APPLICANT: VOSEL, Kurt
APPLICANT: WISS, Markus
TITLE APPLICANT: MYSS, Markus
FILE REFERENCE: Modified Phytases
FILE REFERENCE: Modified Phytases
CURRENT RPLICATION NUMBER: 18/99/044,718
CURRENT FILING DATE: 1998-03-19
FRIOR APPLICATION NUMBER: EP 97810175.6
FRIOR APPLICATION NUMBER: EP 97810175.6
FRIOR FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Talaromyces thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Talaromyces thermophilus
Sequence 8, Application US/09044718; Patent No. 6391605; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6
Best Local Similarity 100.
Matches 6; Conservative
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MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: See figure 19
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VTVSSE 6
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MOLECULE TYPE:
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Patent No. 6838254
GENERAL INFORMATION:
APPLICANT: Raymond HAMERS
APPLICANT: Cecile HAMERS-CASETERMAN
APPLICANT: Serge V. M. MUYLDERWANS
APPLICANT: Serge V. M. WUYLDERWANS
APPLICANT: Cornelis T. VERRIPS
TITLE OF INVENTION: Production of antibodies or (functionalized)
TITLE OF INVENTION: fragments thereof derived from heavy chain immunoglobulins
                                                                                                        APPLICANT: Cecile HAMERS-CASETERMAN
APPLICANT: Serge V. M. WUYLDERMANS
APPLICANT: Serge V. M. WUYLDERMANS
APPLICANT: Leon G. J. FRENKENS
APPLICANT: Cornelis T. VERRIPS
TITLE OF INVENTION: Production of antibodies or (functionalized)
TITLE OF INVENTION: Gragments thereof derived from heavy chain immunoglobulins
TITLE OF INVENTION: of Camelidae
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                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: Pillsbury Madison & Sutro, L.L.P.
STREET: LI00 New York Avenue, N.W.
CITY: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 6; DB 4
100.0%; Pred. No. 2.7
tive 0; Mismatches
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APPLICATION NUMBER: PCT/EP94/01442
FILING DATE: 28-APR-1994
PRIOR APPLICATION NUMBER: BPO 93202079.5
FILING DATE: 15-JUL-1993
PRIOR APPLICATION NUMBER: BPO 93201454.1
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BPO 93201454.1
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BPO 93201239.6
FILING DATE: 29-APR-1993
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,871A
FILING DATE: 29-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                     Sequence 41, Application US/08537871A Patent No. 6838254 GENERAL INFORMATION:
                                                                                          Raymond HAMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.
Matches 6; Conservative
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LENGTH: 16 amino acids
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US-08-537-871A-41
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US-08-537-871A-45
US-08-537-871A-41
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Sequence 35, Application US/08335844A

Sequence 35, Application US/08335844A

Patent No. 6066503

GENERAL INFORMATION:
APPLICANT: GRAHAM, MARGARET
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: NGWYC, JOANIA JANE
APPLICANT: NGWYCON, SUSAN ELIZABETH
APPLICANT: NEWTON, SUSAN ELIZABETH
TITLE OF INVENTION: MAINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
TSTREET: Suite 701-E, 555 Thirteenth St., N.W
STREET: D. CORRESPONDENCE ADDRESSED
STREET: D. CORRESPONDENCE ADDRESSED
STREET: Suite 701-E, 555 Thirteenth St., N.W
STATE: D. CORRESPONDENCE ADDRESSED
                                                                                                                                                                                                                                                       Score 6; DB 2; Length 17; Pred. No. 2.9e+02;
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC Compatible
COMPUTER: Elem PC Compatible
COMPUTER: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,844A
FILING DATE: 09-JAN-1995
CLASSIFICATION: A24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 920936
FILING DATE: 08-MAY-1992
ATONEY/AGENT INFORMATION:
NAME: WALKER, BATDARA
REGISTRATION NUMBER: 35,400
REFERENCE/POCKET NUMBER: 35,400
REGISTRATION INFORMATION:
TELECHONE: (202)783-6040
                                                                                                                                                                                                                                                                        100.0%; Preu. ...
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SEQUENCE CHARACTERISTICS:
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                                                                17 amino acids
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                              single
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MOLECULE TYPE: peptide
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Best Local Similarity
Matches 6; Conserval
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                                                                                                                 STRANDEDNESS:
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US-08-248-839C-53
Sequence 53, Application US/08248839C
Fatent No. 5843701
Fatent No. 5843701
GENERAL INFORMATION:
FAPPLICANT: McConnell, David
APPLICANT: O'Kane, Charles
FITLE OF INVENTION: A Gene Expression System
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 58437020 No. 5843702th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
SITE: New York
CONNTR: USA
CONNTR: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Ind Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast SEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: 15-MAY-1994
CLASSIFICATION NUMBER: 35-127
REFERENCE/DOCKET NUMBER: 35127
REFERENCE/DOCKET NUMBER: 35127
FELECOMMINICATION NUMBER: 35127
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
                 AFFLICATION NUMBER: US/US/J4/,198A
PRILING DATE: 21-NOV-1994
CLASSIFICATION: 424
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/020,526
FILING DATE: 22-FEB-1993
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/761,749
FILING DATE: 17-SEP-1991
PRICA APPLICATION NUMBER: PCT/GB90/00416
FILING DATE: 19-MAR-1990
PRICA APPLICATION NUMBER: PCT/GB90/00416
FILING DATE: 17-MAR-1999
APPLICATION NUMBER: GB 89906156.8
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICATION:
RECERCENCE/DOCKET NUMBER: 36,105
RECECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-500
TELEFAX: 202/638-500
     APPLICATION NUMBER: US/08/347,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
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0; Mismatches 6; Conservative Matches

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Search completed: October 12, 2005, 10:26:31 Job time: 27 secs

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Mus musculus (Mouse)
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q924C7
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Q8HWR5
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Q8HWR9
Q8HWS1
Q8HWS1
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Q8HG1D7
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2: uniprot_trembl:*
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Maximum DB seq length: 35
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SEQUENCE FROM N.A.

MEDLINE=99156934; PubMed=10037744; DOI=10.1074/jbc.274.10.6507;

Kim C.H., Kim H.S., Cubells J.F., Kim K.S.;

"A previously undescribed intron and extensive 5' upstream sequence, but not Phox2a-mediated transactivation, are necessary for high level but not Phox2a-mediated transactivation, are necessary for high level gene!

J. Biol. Chem. 274:6507-6518(1999).

EMBL, AF061198; AAD17521.1;

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-2129/504;
MEDLINE-21292988; PubMed=11262390; DOI=10.1074/jbc.M009382200;
MEDLINE-21292988; Fatall J., Yusta B., Brown T.J., Drucker D.J.;
Lovshin J.A., Estall J., Yusta B., Brown T.J., Drucker D.J.;
"Glucagon-like peptide (GLP)-2 action in the murine central nervous
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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 y Match 0.6%; Score 6; DB 2; Length 18; Local Similarity 100.0%; Pred. No. 1.18+03; hes 6; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last equence update) Norepinephrine transporter (Fragment).
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 039957
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077ZJ1
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Receptor. NON TER SEQUENCE

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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 1.5e+03;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.5e+03;
ative 0; Mismatches 0; Indels
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Swelsen W.T., Voorter C.E., van den Berg-Loonen E.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ316290; CAC87135.1; -.
NON TER
SEQÜENCE 24 AA; 2669 MW; 1942CFC2489CI77F CRC64;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ316288; CAC87133.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Leucocyte antigen (Fragment).
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Name=HLA-B;
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Matches 6; Conservative
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Q8HWR7
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system is enhanced by elimination of GLP-1 receptor signaling."; J. Biol. Chem. 276:21489-21499 (2001).

EMBL; AF318224; AAK63043.1; -. MGD; MGI:2136733; Glp2r.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0004967; F:glucagon receptor activity; TAS.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Pred. No. 1.5e+03;
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Swelsen W.T., Voorter C.E., van den Berg-Loonen E.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databasee.
EMBL; AJ316292; CAC87137.1; -.
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Swelsen W.T., Voorter C.E., van den Berg-Loonen E.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ316291; CAC87136.1; -.
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22 AA; 2526 MW; 2C5BF53DCCD425C9 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MCC antigen (Fragment).
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Leucocyte antigen (Fragment).
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0.6%; Score 6; DB 2; Le:
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0;
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100.0%;
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Best Local Similarity
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24 AA.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                     Query Match 0.6%; Score 6; DB 2; Length 24; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 6; Conservative 0; Mismatches 0; Indels
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ429190; CAD22131.1; -.
NON TER 24 24
SEQÜENCE 24 AA; 2669 MW; 1942CFC2489C177F CRC64;
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24 AA; 2669 MW; 1942CFC2489C177F CRC64;
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1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Leucocyte antigen (Fragment).
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SEQUENCE
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                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                    Swelsen W.T., Voorter C.E., van den Berg-Loonen E.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ316287; CAC87132.1; -.
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Swelsen W.T., Voorter C.E., van den Berg-Loonen B.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ31628; CAC8788.1;
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Swelsen W.T., Voorter C.E., van den Berg-Loonen E.M.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AJ316286; CAC87879.1; -.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
1-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Leucocyte antigen (Fragment).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Leucocyte antigen (Fragment).
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Name=HLA-B;
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08HWS1
1D 08HW
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Indels
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TISSUB-PETLY blood;
Swelsen W.F., Voorter C.E., van den Berg-Loonen B.M.;
Swelsen W.F., Voorter C.E., van den Berg-Loonen B.M.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ417674; CAD1046.1; -.
NON TER 24
SEQUENCE 24 AA, 2669 MW; 1942CFC2489C177F CRC64;
                                                                                                                                                                                                                                                                                                     01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
MHC class I antigen (Fragment).
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Best Local Similarity 100.
Matches 6; Conservative
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Amphibian defense peptide; Antibiotic; Direct protein sequencing;
                                                                   6; Conservative
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                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                            UL15 protein (Fragment).
Name=UL15;
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                                                                                         878 KVLKAA 883
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                                                       Best Local Similarity
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Eur. J. Blochem. 219:145-154(1994).
-!- FUNCTION: Possesses a potent antimicrobial activity against
bacteria, fungi and protozoa. Probably acts by disturbing membrane
functions with its amphipatic structure.
-!- SUBCELDIDAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
-!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
Dermaseptin subfamily.
                                                                                                                                               SEQUENCE.
MEDLINE=99259579; PubMed=10327595; DOI=10.1016/S0305-0491(98)10144-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                 -1- FUNCTION: Hemocyanins are copper-containing oxygen carriers occurring freely dissolved in the hemolymph of many mollusks and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DMS4_PHYSA STANDARD; PRT; 27 AA.
P80280;
D1-FBB-1994 (Rel. 28, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Dermaseptin 4 (DS IV).
Phyllomedusa sauvagei (Sauvage's leaf frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Annra; Neobatrachia; Hyloidea; Hylidae;
                                                                                                                                                                                                                                                                                           InterPro; IPR000896; Hemocyanin.
InterPro; IPR00227; Tyrosinase.
PROSITE; PS00209; HEMOCYANIN 1; PARTIAL.
PROSITE; PS00497; TYROSINASE 1; PARTIAL.
PROSITE; PS00497; TYROSINASE 1; PARTIAL.
COPPER; DS00498; TYROSINASE 2; PARTIAL.
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                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Extracellular.
-i- TISSUE SPECIFICITY: Hemolymph.
-i- SIMILARITY: Belongs to the tyrosinase family. Hemocyanin
                  Stoeva S., Dolashka P., Hristova R., Genov N., Voelter W.; "Subunit composition and N-terminal analysis of arthropod
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.6%; Score 6; DB 1; Length 26; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 6; Conservative 0; Mismatches 0; Indels
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             26 AA
                                                                                                                                                                                                      Biochem. Physiol. 122B:69-75(1999)
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MEDLINE=94139686; PubMed=8306981;
Mor A., Nicolas P.;
             STANDARD;
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                                                                                                                                                                                            hemocyaning.";
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SEOUENCE
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  HCY3 HOMAM
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Carter E.P., Umenishi F., Matthay M.A., Verkman A.S.;

"Increased water permeability across the blood-gas barrier in rabbit lungs in the first 24 hours after birth.";

J. Clin. Invest. 0:0-0(1997).

EMBL; AF000313; AAB94410.1; -.

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NON_TER 31 31

SEQÜENCE 31 AA; 3525 MW; F80D65C92838FA92 CRC64;
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
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100.0%; Pred, No. 1.7e+03;
tive 0; Mismatches 0; Indels
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                                                                         DB 1; Length 27;
Fungicide; Multigene family.
SEQUENCE 27 AA; 2779 MW; 43C94D2DC19721A8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Beta-adgins (Fragment)
Oryctolagins cuniculus (Rabbit).
                                                                         0.6%; Score 6; DB 1; Ler
100.0%; Pred. No. 1.6e+03;
rative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                           28 AA
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InterPro; IRR003499; DNA pack N.
Pfam; PFC2500; DNA_pack N. 1.
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05-JUL-2004 (TrEMBLrel. 27, Created)
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Query Match 0.6%; Score 6; DB 2; Length 31; Best Local Similarity 100.0%; Pred. No. 1.8e+03; Matches 6; Conservative 0; Mismatches 0; Indels

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136 DIRKDL 141 |||||| 24 DIRKDL 29

à **Q**.

Search completed: October 12, 2005, 10:25:21 Job time : 69 secs

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October 12, 2005, 10:19:24; Search time 21 Seconds (without alignments) 4911.637 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 MAPPIGVLSSLLLLVTIAGC......VSMNGSIRNGASFSYCSKDR 1072 US-10-764-390-3 Perfect score: Scoring table: Sequence: Title:

OLIGO Gapop 60.0 , Gapext 60.0

283416 seqs, 96216763 residues Searched:

0

Word size:

7756 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 35

Post-processing: Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Blatio	IS1/cat protein -	hemocyanin M3' - c		placental lactogen	Ig heavy chain CRD	Ig heavy chain CRD	glutathione peroxi	hypothetical prote	T-cell antigen rec	Na+/K+-exchanging	hypothetical prote	Ig heavy chain V r	Ig heavy chain J r	T-cell receptor al	н	Ig heavy chain J r	26K kidney and gal	one tra	Ig heavy chain J r	Ig heavy chain J r	cell receptor	Ig heavy chain J r		protein-tyrosine k	Ig heavy chain J-H	anti-angiotensin,	T-cell receptor be	T-complex protein
SUMMARIES	EI EI	5593	153186	G60529	A21440	A47364	PT0255	PT0319	A38929	809395	S47377	S29878	S27140	S26791	PS0382	G41299	F28587	PS0383	D58501	C37520	S26747	S26744	124687	PS0384	A49237	S24780	A25941	139461	388	828396
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Ig heavy chain CRD cytochrome P450 PB malate dehydrogena	equinatoxin 1C - s 2-halobenzoate 1,2 dTDPQIOCOSE 4,6-de	coenzyme r420 nyur tenebrosin B - sea RNA-binding protei duodenase - bovine	110K ATPase, intes ribosomal protein alpha-1-antichymot	Ig heavy chain DJ Kinetoplast DNA-as hemocyanin 1 - edi
PT0332 A60822 S04961	PC1151 B44920 B44835	S63483 B34016 B46174 S69371	A61487 S29858 IS4268	PH1333 D47256 A60529
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ALIGNMENTS

RESULT 1 855937 translation initiation factor eIF-4E - fruit fly (Drosophila melanogaster) (fragments) C.Species: Drosophila melanogaster
 Cjbate: 27-OCT-1995 #sequence_revision 03-NOV-1995 #text_cnange 09-001-2004 C;Accession: 855937 R;Hernandez, G.; Sierra, J.M. Biochim. Biophys. Acta 1261, 427-431, 1995
A;Title: Translation initiation factor eIF-4E from Drosophila: cDNA sequence and express A;Reference number: S55936; MUID:95260867; PMID:7742371 A;Accession: S55937
A;Status: preliminary A;Molecule type: protein A;Residues: 1-8;9-27;28-32 <her> A;Cros-references: UNIPROT:OYMAE6</her>
 C,Genetics: A,Gene: FlyBase:E1f4F A,Cross-references: FlyBase:FBgn0013947 C,Superfamily: translation initiation factor eIF-4E
 Query Match 0.6%; Score 6; DB 2; Length 32; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

307 PPTSAA 312 PPTSAA 26 21 셤 à

Listuce is scherichia coli (fragment)
C;Species: Bacherichia coli
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C;Species: Bacherichia coli
C;Species: Bacherichia coli
C;Species: Bacherichia coli
C;Accession: 153186; I66659
R;Lida, S.; Marcoli, R.; Bickle, T.A.
E,Mancoli, E,Mancoli, R.; Bickle, T.A.
E,Mancoli, E,Mancoli, R.; Bickle, MUID:84236045; PMID:6329702
A;Residues: L-33 «RES»
A;Cross-references: UNIPROT:Q52315; GB:M24180; NID:g151758; PIDN:AAA26059.1; PID:g151759
A;Schaus: preliminary; translated from GB/EMBL/DDBJ
A;Schaus: preliminary; translated from GB/EMBL/DDBJ
A;Schaus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-18, 'G' «RE2»
A;Cross-references: GB:M24181; NID:g151760; PIDN:AAA26060.1; PID:g151761

Query Match 0.6%; Score 6; DB 2; Length 33; Best Local Similarity 100.0%; Pred. No. 2.9e+02;

6; Conservative

Matches

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C.Species: Homo sapiens (man)
C.Species: Jo.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C.Accession: Pr0319
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A.Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J.
A.Reference number: PT0222; MUID:91108337; PMID:1899102
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
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h 0.5%; Score 5; DB 2; Length 10; Similarity 100.0%; Pred. No. 1.1e+03; 5; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.3e+03;
rative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-12 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: B lymphocyte C; Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 100.
Matches 5; Conservative
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-13 <GET>
           Query Match
Best Local Similarity
Matches 5; Conserv
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A; Residues: 1-12 < YAM>
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A47364
placental lactogen-I precursor - mouse (fragment)
placental lactogen-I precursor - mouse (fragment)
c;Species: Mus sp. (mouse)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996
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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996
C;Date: 12-Aug-1996
Milliance in Aug-1996
A;Reterence muser: A47364; MUID: 93225959; PMID: 8469232
A;Residues: Dreliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 eRES>
A;Cross-references: GB:S58124; NID: 9299449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Cherax destructor (yabby)
C;Species: Cherax destructor (yabby)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C;Accession: G60529
R;Neuteboom, B.; Sierdsema, S.J.; Beintema, J.J.
Comp. Biochem. Physiol. B 94, 587-592, 1989
A;Title: The relationship between N-terminal sequences and immunological characterizatic
A;Reference number: A60529; MUID:90151075; PMID:2620501
A;Recession: G60529
A;Accession: G60529
A;Accession: G60529
A;Accession: G10529
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C; Species: Trypanosoma brucei
C; Species: Trypanosoma brucei
C; Species: Trypanosoma brucei
C; Species: Trypanosoma brucei
C; Accession: A21440
R; Parsons, M.; Nelson, R.G.; Watkins, K.P.; Agabian, N.
Cell 38, 309-316, 1984
A; Title: Trypanosome mRNAs share a common 5' spliced leader sequence.
A; Reference number: A90853; MuID:84282716; PMID:6088073
A; Reference number: A90853; MuID:84282716; PMID:6088073
A; Residues: 1-8 - PRR>
A; Residues: 1-8 - PRR>
A; Residues: 1-8 - RPR>
A; Cross-references: UNIPROT:P22225; GB:K02195; NID:g162150; PID:g162151
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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hemocyanin M3' - cray£ish (Cherax destructor) (fragment)
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6; Conservative

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Query Match

900 FLLFKV 905

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C;Accession: S27140
R;Keaveney, M.; Klug, J.; Gannon, F.
NAS Seq. 2, 347-358, 1992
A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene A;Reference number: S27140; MUID:93075998; PMID:1476547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (N63P2) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 02-Aug-1996 #text_change 20-Jun-2000
C;Accession: 525791; S19879
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Rim. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami A;Reference number: S26786; MUID:92111632; PMID:1730251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X61022; NID:g32791; PIDN:CAA43356.1; PID:g1335124; EMBL:X61234; C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain J region 2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 06-Jun-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 05-Mar-1994 #sequence_revision 12-May-1995 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-14 «KEA»
A;Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44319.1; PID:g31202
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100.0%; Pred. No. 1.5e+03;
7ative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0;
                          A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-14 < LYT>
A,Cross-references: UNIPROT:Q7M0G4
C,Keywords: hydrolase
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Best Local Similarity 100.0
Matches 5; Conservative
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A; Residues: 1-15 < MOR>
  A;Accession: S29878
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"Species: Drosophila melanogaster (Species: Drosophila melanogaster)

C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997

C;Accession: S09395

K;Gisselmann, G:, Sewing, S:, Madsen, B.W.; Mallart, A.; Angaut-Petit, D.; Mueller-Holtk

EMBO J. 8, 2359-2364, 1989

A;Fitle: The interference of truncated with normal potassium channel subunits leads to a A;Feference number: S09395; MUID:90005442; PMID:2551680

A;Accession: S09395

A;Accession: S09395

A;Ketus: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 cGIS>
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Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha-2 chain - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: $29878

R;Lytton, J.

Biochem. Biophys. Res. Commun. 132, 764-769, 1985

A;Title: The catalytic subunits of the (Na(+), K(+))-ATPase alpha and alpha(+) isozymes

A;Reference number: $29877; MUID:86050667; PMID:2998384
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A; Accession: 847377
A; Status: preliminary
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C;Species: Homo sapiens (man)
C;Decies: Homo sapiens (man)
C;Decies: Moo.Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47377
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-13 - 4.LEH>
A;Cross=references: EMBL: 235706; NID: 9527505; PIDN: CAA84775.1; PID: 9527506
C;Keywords: T-cell receptor
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100.0%; Pred. No. 1.4e+03;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.4e+03;
ative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0;
A;Cross-references: UNIPROT:Q7M355
C;Superfamily: glutathione peroxidase
C;Keywords: oxidoreductase
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C;Accession: PS0382
R;Lang, P.; MocIkat, R.
R=101264, 1991
A;Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse and A;Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse and A;Reference number: JH0666; MUD:91340162; PMID:1908401
A;Accession: PS0382
A;Accession: PS0382
A;Residues: 1-15 < LAN>
A;Residues: 1-15 < LAN>
CS08202131; Immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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G41299

C; Cell receptor alpha chain precursor J region (39) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 05-Nov-1999
C; Accession: G41299
R; Wematsu, Y:, Wege, H:; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G.; Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991
A; Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheumatc A; Accession: G41299
A; Reference number: A41299; MUID:92020887; PMID:1656449
A; Residues: preliminary
A; Molecule type: mRNA
A; Messidues: 1-15 < UEM-A; MAResidues: 1-15 < UEM-A; MAResidues: T-cell receptor
C; Keywords: T-cell receptor
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 0;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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Adro0790
Adro0811
Adro0844
Adro0639
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                                                         ADRO0639
ADR00643
ADR00648
ADR00656
ADR00671
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ADRO0689
ADRO0694
ADRO0721
ADRO0741
ADRO0769
ADRO0760
ADRO0760
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ADR00844
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23-AUG-2000; 2000US-00649167.
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    Tang
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N-PSDB; AAS86253.
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    WO200175067-A2.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New 254PID6B BIRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PID6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a 254P1D6B small interfering RNA (siRNA)
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                              100.0%; Pred. ...
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100.0%; Pred. No.
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Perez-Villar JJ, Faris M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human 254P1D6B peptide SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR00632 standard; peptide; 16 AA.
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                  Sequence 19 AA;
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that encodes the protein; (3) a composition comprising a polynucleotide that that full complement of the polynucleotide described above; (4) (generating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PloBB-related protein or a 254PloBB-related protein or a 254PloBB-related protein or a 254PloBB-related protein or a 254PloBB-related protein or a 254PloBB-related protein or a 254PloBB-related protein or a 254PloBB-related protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and contract or a diagnostic agent, reproduction or survival of cancer cells that express the protein of P1. 254PloBB has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PloBB gene is located on chromosome 6p22.
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254PID6B-related protein; cytostatic; gene therapy; cancer; human;
254PID6B v.3; chromosome 6.
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 16;
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Pred. No. 2.1e-07;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR00854 standard; peptide; 24 AA.
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Perez-Villar JJ, Faris
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 16 AA;
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consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pt. see SEQ ID NO:3, 5 or 7 ADR00592, ADR00596, or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein cany of the test 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99* homologous or identical to an entire amino acid sequence of P1; (2) a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide that encodes the protein of the polymucleotide described above; (4) generating a mammalian immune response directed to the protein or a 254PID6B-related polymucleotide; (6) a composition that modulates the status of a cell that expresses a protein of P1; (7) a pharmaceutical composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; a non-human transgenic animal that produces the antibody; (10) a composition and administration of P1; (7) a pharmaceutical correction of a protein of P1; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a chypridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PID6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents a human 254PID6B v.3 peptide, which is used in the exemplification of the present invention. The human 254PID6B gene is located on chromosome 6p22.
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Sequence 24 AA;

Gapв ö 1.3%; Score 14; DB 8; Length 24; 100.0%; Pred. No. 2.6e-05; ive 0; Mismatches 0; Indels 20 CARKQCSEGRTYSN 33 14; Conservative Query Match Best Local Similarity Matches ਨੇ

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11 CARKQCSEGRIYSN 24

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ADR00851 standard; peptide; 29 AA. RESULT 4
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Human 254PlD6B v.2 peptide SEQ ID NO:262. (first entry) 04-NOV-2004 ADR00851;

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.2; chromosome 6.

Homo sapiens

WO2004067716-A2.

12-AUG-2004.

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P.

(AGEN-) AGENSYS INC.

Ge ₩; Kanner SB, Raitano AB, Jakobovits A, Challita-Bid PM, Perez-Villar JJ, Faris M;

WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Example 13; SEQ ID NO 262; 345pp; English.

The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence witch encodes the couples protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous continuous amino acids of a protein of figure 2 (PI), see SEQ ID COMBISTS essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (PI), see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein contiguous amino acids sequence of PI; (2) a polymucleotide that encodes the protein; (3) a composition comprising a polymucleotide contexting a mammalian immune response directed to the protecin of PI; (5) detecting, in a sample, the polymucleotide described above; (4) contexting in a sample, the presence of a 254PlD6B-related polymucleotide; (6) a composition that modulates the crapos directed to the protein or a 254PlD6B-related polymucleotide; (6) a composition that modulates the composition that comprises the composition described above in a human composition that comprises the composition described above in a human composition that comprises the composition are surfibed above in a human composition of prices of composition of prices of context of protein of PI; (7) a pharmaceutical composition of prices of context of protein of PI; (1) inhibiting growth, reproduction or survival of cancer cells that express the protein of PI; (1) inhibiting growth, reproduction or survival of cancer cells that express the protein of PI; (1) inhibiting and detecting cancer. The present sequence correction of the human 254PlD6B v.2 peptide, which is used in the exemplification of the process of the protein of the protein of the protein of the protein of the protein of pricesent invention. The human 254PlD6B gene is located on chrom ö Gaps ö Length 29; 0; Indels 1.3%; Score 14; DB 8; Le 100.0%; Pred. No. 3.1e-05; tive 0; Mismatches 0; ADR00857 standard; peptide; 29 AA. 143 FLGKDWGLEEMSEY 156 1 FLGKDWGLEEMSEY 14 04-NOV-2004 (first entry) Query Match
Best Local Similarity 100.
Matches 14; Conservative Sequence 29 AA; ADR00857; ADR00857 ID ADR(RESULT 5 a 8

Human 254P1D6B v.5 peptide SEQ ID NO:268.

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; 254P1D6B v.5; chromosome 6.

Homo sapiens

12-AUG-2004.

WO2004067716-A2

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P

(AGEN-) AGENSYS INC.

3 e Challita-Eid PM, Jakobovits A, Kanner SB, Raitano AB, Ja Perez-Villar JJ, Faris M;

WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that

Ge ₩;

Challita-Eid PM,

Jakobovits A,

Perez-Villar JJ, Faris M;

Raitano AB,

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the controlled stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous in length. Also described. (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADRO0594). ADRO0596, or a peptide in nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADRO05952, ADRO0596, or a peptide in namy of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99‡ homologous or that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99‡ homologous or identical to an entire amino acid sequence of Pl; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of Pl; (5) generating a mammalian immune response of a 254P1D6B-related protein or a 254P1D6B-related polynucleotide; (6) a composition that modulates the statut dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the antibody; (10) a non-human transgenic animal that produces the animal transfer animal that produces the animal animal transgenic animal that produces the animal animal transgenic animal that produces the animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal a
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s to the nucleic acid ORF sequence which encodes the 254PlD6B corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                               Example 13; SEQ ID NO 268; 345pp; English.
                                                                                 and treating cancer.
    corresponds to
                                                 protein
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Gaps ö 1.3%; Score 14; DB 8; Length 29; 100.0%; Pred. No. 3.1e-05; ative 0; Mismatches 0; Indels 128 GIWGDSPEDIRKDL 141 Query Match
Best Local Similarity 100.
Matches 14; Conservative Sequence 29 AA; 8

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1 GIWGDSPEDIRKDL 14 ADR00673; RESULT 6

Human 254P1D6B peptide SEQ ID NO:84. ADR00673 standard; peptide; 9 AA. (first entry) 04-NOV-2004 XBXBXBXBXSXEXEXBXBXBXBX

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; chromosome 6.

Homo sapiens,

WO2004067716-A2. 12-AUG-2004

23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P. (AGEN-) AGENSYS INC

or a diagnostic agent to a cell that expresses the protein of PI; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of PI. 254PLD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PLD6B peptide, which is used in the exemplification of the present invention. The human 254PLD6B gene is located on chromosome 6p22. Example 9; SEQ ID NO 84; 345pp; English. protein or correspon and treating cancer. Sequence 9 AA;

0.8%; Score 9; DB 8; Length 9; 100.0%; Pred. No. 1.80+06; ive 0; Mismatches 0; Indel 9; Conservative 320 ELPISPITA 328 σ Local Similarity Query Match Best Loca Matches ઠ 셤

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254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; Human 254PlD6B peptide SEQ ID NO:131. ADR00720 standard; peptide; 9 AA. (first entry) 04-NOV-2004 ADR00720; ADR00720

WO2004067716-A2. chromosome 6. Homo sapiens

12-AUG-2004.

Ge ≅;

Jakobovits A, Challita-Eid PM,

(AGEN-) AGENSYS INC

12-AUG-2004

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New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
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                                                                                                                                    24-JAN-2003; 2003US-0442526P.
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Perez-Villar JJ, Faris M;
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      Homo sapiens.
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                                                                                                                                                                                                                                                                                                              composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the C254F1D6B protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous an encodes in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (PI, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of PI; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein of PI; (5) detecting, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related protein or a 254PlD6B-related protein or a composition that modulates the composition that comprises the composition described above in a human cunt dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgant animal that produces the antibody; (10) a non-human transgant animal that produces the antibody; (10) a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                                                                                                                                                                                 New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                    The present invention describes a 254P1D6B small interfering RNA (siRNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that
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                                                                                                 Raitano AB, Jakobovits A, Challita-Eid PM, r JJ, Faris M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Pred. No.
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23-JAN-2004; 2004WO-US001965.
                                 24-JAN-2003; 2003US-0442526P.
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                                                                  (AGEN-) AGENSYS INC.
                                                                                                                                                  WPI; 2004-580991/56.
                                                                                                                                                                                                                                  treating cancer.
                                                                                                               Perez-Villar JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9 AA;
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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the cast be nucleotides in length. Also described: [1] a composition that comprises, cucleotides in length. Also described: [1] a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID ONC), So 7 ABR00999, ABR00999, or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein canny of the 42 lists of peptides, given in the specification, or a protein canny of the 42 lists of peptides, given in the specification or a protein canny of the 42 lists of peptides, given in the specification or a protein canny of the 42 lists of peptides, given in the specification or a protein canny of the sample amino acid sequence of Pl; (2) a polymucleotide that is a full complement of the polymucleotide described above; (4) detecting, in a sample, the presence of a 254P1D6B-related protein or a 254P1D6B-related polymucleotide; (6) a composition that modulates the composition that comprises the composition described above in a human cuit dose form; (8) an antibody or its fragment, which is monoclonal; (9) which shams transgenic animal that produces the antibody; (10) a pharmacturical and antibody or its fragment, which is monoclonal; (9) which shams transgenic animal that produces the antibody; (10) a pharmacturical animal transgenic animal that produces the antibody; (10) a pharmacturical animal transgenic animal that produces the antibody; (10) a pharmacturical animal transferince animal that produces the antibody; (10) a pharmacturical animal transferince animal that produces the animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal anim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hybridoma that produces the antibody; (11) delivering a cytotoxic agent
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No. 1.8e+06;
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100.0%; Pred. No. 1.8
tive 0; Mismatches
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les 9; Conserv
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Matches
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254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human;

Human 254P1D6B peptide SEQ ID NO:170

04-NOV-2004 (first entry)

ADR00759;

ADR00759 standard; peptide; 9 AA.

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The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence withch encodes the cast double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous cullectides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID CON 31, 5 or 7 ARR00522, ARR00594 or ARR00596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein can or or any of the 42 lists of peptides, given in the specification, or a protein can or or or any of the 42 lists of peptides, given in the specification, or a protein can or or or a composition acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) a canting a mammalian immune response directed to the protein of P1; (5) a generating a mammalian immune response directed to the protein or a castplo6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition that modulates the composition that comprises the composition does form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a pharmaceutical continual dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a pharmaceutical continual dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a pharmaceutical continual dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the animal dose form; (8) and antibody or its fragment.
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                                                                                               254PID6B; small interfering RNA; siRNA; immune response;
254PID6B-related protein; cytostatic; gene therapy; cancer; human;
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100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0; Indel
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Human 254PlD6B peptide SEQ ID NO:157
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Best Local Similarity luv...
Pest Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AGEN-) AGENSYS INC
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                                                                                                                                                                                                                    chromosome 6.
                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting

Example 9; SEQ ID NO 170; 345pp; English.

and treating cancer.

Ge ₩;

Challita-Eid PM,

Perez-Villar JJ, Faris M;

WPI; 2004-580991/56.

(AGEN-) AGENSYS INC.

23-JAN-2004; 2004WO-US001965. 24-JAN-2003; 2003US-0442526P

WO2004067716-A2

12-AUG-2004.

chromosome 6. Homo sapiens.

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The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PlD6B protein, or corresponds to a subsequence of the ocodes the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists of a peptide of eight, nine, ten, or consists sesentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 [PL, see SEQ ID NO.3, 5 or 7 ADROGS92, ADROGS94 or ADROGS96), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein CC that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of P1; (2) a polynucleotide that is a full complement of the polynucleotide described above; (4) generating a mammalian immune response directed to the protein or a cereating a mammalian immune response directed to the protein of P1; (5) detecting, in a sample, the presence of a 254PlD6B-related protein or a 254PlD6B-related polynucleotide; (6) a composition that modulates the composition that comprises the composition described above; (10) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses a protein of P1; (7) a pharmaceutical count dome form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and correct cells that expresses the protein of P1; and correct cells that cypresses the protein of P1; and correct or a diagnostic agent, reacting and detecting one survival of cancer cells that expresses the protein of P1; and correct ing cancer the man 254PlD6B genetic invention or survival of cancer cells the human 254PlD6B genetics or survival or capresent invention. The human 254
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Matches 9; Conservative
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47 RVSHTFPVV 1 RVSHTFPVV

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RESULT 10 ADR00759

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1 PTPPTSAAP 9
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ADR00767 standard; peptide; 9 AA. RESULT 11

ADR00767;

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> (first entry) 04-NOV-2004

Human 254P1D6B peptide SEQ ID NO:178.

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; chromosome 6.

Homo sapiens

WO2004067716-A2.

12-AUG-2004.

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P.

(AGEN-) AGENSYS INC.

Ge W; Challita-Eid PM, Jakobovits A, Perez-Villar JJ, Faris M; Raitano AB,

WPI; 2004-580991/56.

New 254P1D6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

Example 9; SEQ ID NO 178; 345pp; English.

New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting

Example 9; SEQ ID NO 208; 345pp; English.

and treating cancer.

The present invention describes a 254PID6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the controlled solid open reading frame (ORF) sequence which encodes the controlled siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous mucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADRO0592, ADRO0594 or ADRO0596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein control to an entire amino acid sequence of Pl; (2) a polymucleotide that is a full complement of the polymucleotide described above; (4) centraling in a sample, the presence of Pl; (2) a polymucleotide that is a full complement of the polymucleotide described above; (4) centraling in a sample, the presence of a 254PID6B-related protein or a 254PID6B-related polymucleotide; (6) a composition that modulates the composition that comprises the composition described above in a human unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that expresses the antibody; (10) a non-human transgenic animal that expresses the antibody; (10) a protein of price of a control of prices the antibody; (10) a non-human transgenic animal that expresses the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254P106B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254P106B peptide, which is used in the exemplification of the present invention. The human 254P106B gene is located on chromosome 6p22.

The present invention describes a 254P1D6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the cast the nucleic acid open reading frame (ORF) sequence of the ORF, where the 254P1D6B protein, or corresponds to a subsequence of the ORF, where the caption or corresponds to a subsequence of the ORF, where the couple stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous consists a sesentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID CC NO:3, 5 or 7 ADRO652, ADRO6594 or ADRO6596), or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein control of that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or that tencodes the protein; (3) a composition comprising a polymucleotide that is a full complement of the polymucleotide described above; (4) generating a mammalian immune response directed to the protein of a 254P1D6B-related polymucleotide; (6) a composition that modulates the composition that modulates the composition that comprises the composition described above in a human continuant transgent animal that produces the antibody; (10) a pnarmaceutical continuant transgent animal that produces the antibody; (10) a composition of a continuant animal that produces the antibody; (10) a pnarmaceutical continuant transgent animal that produces the antibody; (10) a pnarmaceutical continuant transgent animal that produces the animal animal transgent animal that produces the animal animal transgent animal that produces the animal animal transgent animal that produces the animal animal transgent animal that produces the animal animal transgent animal that produces the animal animal transgent animal that produces the animal animal transgent animal that produces the animal animal animal transfer the animal animal transfer the animal animal animal animal animal animal

hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of P1; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of P1. 254PID6B has cytostatic activity, and can be

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Ä Sequence 9

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                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                            254P1D6B; small interfering RNA; siRNA; immune response;
254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kanner SB, Raitano AB, Jakobovits A, Challita-Eid PM,
Perez-Villar JJ, Faris M;
                                                  0; Indels
                Length 9;
                  DB 8; Le:
                0.8%; Score 9; DB 8
100.0%; Pred. No. 1.8
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                          Human 254P1D6B peptide SEQ ID NO:208.
                                                                                                                                                                                                                ADR00797 standard; peptide; 9 AA.
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Query Match
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                                                                                                                      1 PVETTYNYE
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                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                              RESULT 12
                                                                                                                                                                                               ADR00797
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The present invention describes a 254PlD6B small interfering RNA (siRNA) composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the couble stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (Pl, see SEQ ID NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of Pl; (2) a polymucleotide that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or identical to an entire amino acid sequence of Pl; (2) a polymucleotide that is a full complement of the polymucleotide described above; (4) generating a mammalian immune response directed to the protein or a captured polymucleotide; (6) a composition that modulates the capture of a cell that expresses a protein of Pl; (7) a pharmaceutical composition that comprises the composition described above in a human
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used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254P1D6B peptide, which is used in the exemplification of the present invention. The human 254P1D6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New 254PID6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PiD6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.
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254PID6B-related protein; cytostatic; gene therapy; cancer; human;
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                                                                                                                                   DB 8; Length 9; . 1.8e+06;
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                                                                                                                                   0.8%; Score 9; DB 8
100.0%; Pred. No. 1.8
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 254P1D6B peptide SEQ ID NO:210.
                                                                                                                                                                                                                                                                                                                                                    ADR00799 standard; peptide; 9 AA.
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                                                                                                                                                                          9; Conservative
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Perez-Villar JJ, Faris
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Best Local Similarity
Matches 9; Conserv
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                                                                                               Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome 6.
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composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PDOBS protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or eleven contiguous amino acids of a protein of figure 2 (PI). No.3, 5 or 7 ADRO0594, ADRO0595, or a peptide included in any of the 42 lists of peptides, given in the specification, or a protein identical to an entire amino acid sequence of PI; (2) a polynucleotide that encodes the protein; (3) a composition comprising a polynucleotide
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unit dose form; (8) an antibody or its fragment, which is monoclonal; (9) a non-human transgenic animal that produces the antibody; (10) a hybridoma that produces the antibody; (11) delivering a cytotoxic agent or a diagnostic agent to a cell that expresses the protein of Pi; and (12) inhibiting growth, reproduction or survival of cancer cells that express the protein of Pi. 254PlD6B has cytostatic activity, and can be used in gene therapy. The compositions, molecules and methods are useful for treating and detecting cancer. The present sequence represents the human 254PlD6B peptide, which is used in the exemplification of the present invention. The human 254PlD6B gene is located on chromosome 6p22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New 254PiD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PiD6B protein or corresponds to a subsequence of the ORF, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a 254P1D6B small interfering RNA (siRNA)
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254PID6B-related protein; cytostatic; gene therapy; cancer; human;
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Pred. No. 1.8e+06;
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100.0%; Pred. No....
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 254PlD6B peptide SEQ ID NO:246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR00835 standard; peptide; 9 AA.
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Matches 9; Conservative
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                                                                                                                                                                                                                    Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR00835;
                                                                                                                                                                                                                                                        Query Match
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that is a full complement of the polynucleotide described above; (4)
generating a mammalian immune response directed to the protein of Pl; (5)
detecting, in a sample, the presence of a 254PloBe-related protein or a
254PloBe-related polynucleotide; (6) a composition that modulates the
status of a cell that expresses a protein of Pl; (7) a pharmaccutical
composition that comprises the composition described above in a human
unit dose form; (8) an antibody or its fragment, which is monoclonal; (9)
a non-human transgenic animal that produces the antibody; (10) a
a non-human transgenic animal that produces the antibody; (10)
a diagnostic agent to a cell that expresses the protein of Pl; and
(12) inhibiting growth, reproduction or survival of cancer cells that
express the protein of Pl. 254PlDB has cytostatic activity, and can be
used in gene therapy. The compositions, molecules and methods are useful
contracting and detecting cancer. The present sequence represents the
human 254PlDGB peptide, which is used in the exemplification of the
present invention. The human 254PlDGB gene is located on chromosome 6p22. Sequence 9 AA; \$

0; Indels 0.8%; Score 9; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; 100.0%; Pred. nc. Best Local Similarity 100. Matches 9; Conservative 558 QIVLYEWSL 566 σ Query Match ð

Gaps

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ADR00645

Human 254PlD6B peptide SEQ ID NO:56. ADR00645 standard; peptide; 9 AA. (first entry) 04-NOV-2004 ADR00645;

254P1D6B; small interfering RNA; siRNA; immune response; 254P1D6B-related protein; cytostatic; gene therapy; cancer; human; chromosome 6.

Homo sapiens.

WO2004067716-A2.

12-AUG-2004.

23-JAN-2004; 2004WO-US001965.

24-JAN-2003; 2003US-0442526P.

(AGEN-) AGENSYS INC.

Ge ≅ Jakobovits A, Challita-Eid PM, Kanner SB, Raitano AB, J Perez-Villar JJ, Faris M; WPI; 2004-580991/56.

Example 9; SEQ ID NO 56; 345pp; English.

New 254PlD6B siRNA composition comprising a double stranded siRNA that corresponds to the nucleic acid ORF sequence which encodes the 254PlD6B protein or corresponds to a subsequence of the ORF, useful for detecting and treating cancer.

composition that comprises a double stranded siRNA that corresponds to the nucleic acid open reading frame (ORF) sequence which encodes the 254PlDGB protein, or corresponds to a subsequence of the ORF, where the double stranded siRNA is 19, 20, 21, 24, or 25 contiguous nucleotides in length. Also described: (1) a composition that comprises, consists essentially of, or consists of a peptide of eight, nine, ten, or The present invention describes a 254PlD6B small interfering RNA (siRNA)

c eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID
NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596, or a peptide included in
the 42 lists of peptides, given in the specification, or a protein
that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or
identical to an entire amino acid sequence of P1; (2) a polymucleotide
that encodes the protein; (3) a composition comprising a polymucleotide
that is a full complement of the polymucleotide described above; (4)
generating a mammalian immune response directed to the protein of P1; (5)
generating a mammalian immune response directed to the protein of P1; (5)
generating, in a sample, the presence of a 254PD6B-related protein or a
254PD6B-related polymucleotide; (6) a composition that modulates the
status of a cell that expresses a protein of P1; (7) a pharmaceutical
composition that comprises the composition described above in a human
unit dose form; (8) an antibody or its fragment, which is monoclonal; (9)
a non-human transgenic animal that produces the antibody; (10) a
hybridoma that produces the antibody; (11) delivering a cytotoxic agent
corresponded the protein of P1. 254PlD6B has cytostatic activity, and can be
used in gene therapy. The compositions, molecules and methods are useful
for treating and detecting cancer. The present sequence represents the
human 254PlD6B peptide, which is used in the exemplification of the
present invention. The human 254PlD6B gene is located on chromosome 6p22.

Sequence 9 AA;

Gaps ö 0; Indels 0.8%; Score 9; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; tive 0; Mismatches 0; Indelk Query Match 0.8 Best Local Similarity 100. Matches 9; Conservative

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Search completed: October 12, 2005, 10:24:01 Job time : 74 secs

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Sequence 261, App
Sequence 261, App
Sequence 43, Appl
Sequence 266, Appl
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Sequence 266, Appl
Sequence 255, Appl
Sequence 118, Appl
Sequence 118, Appl
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| Cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

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Sequence 268, Application US/10764390

Sequence 268, Application US/10764390

Sequence 268, Application Wol0214212A1

GENERAL INFORMATION:
APPLICANT: Balensye, Inc.
APPLICANT: Generation, Arbur B.
APPLICANT: Jakobovites, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Breven B. Kanner:
TITLE OF INVENTION: Derez-Villar
TITLE OF INVENTION: Baltitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer:
TITLE OF INVENTION: Cancer:
TITLE OF INVENTION: Cancer:
TITLE OF INVENTION: Cancer:
TITLE OF INVENTION: Cancer:
FILE REFERENCE: 51158-20081.00

CURRENT APPLICATION NUMBER: US60/442,526

PRIOR APPLICATION NUMBER: US60/442,526

PRIOR APPLICATION NUMBER: US60/442,526

NUMBER OF SEQ ID NOS: 277

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 29

TYPE: PRT

ORGANISM: Homo sapiens
US-10-764-390-268

Query Match
Best Local Similarity 96.6%; Pred, No. 0.0062;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Gaps

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Indels

1;

0; Mismatches

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18; Conservative
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Matches 18; Conser
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LENGTH: 16
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Publication No. US20040214212A1

GENERAL INFORMATION:

APPLICANT: Agensys, Inc.

APPLICANT: Agensys, Inc.

APPLICANT: Callita-Eid, Pia M.

APPLICANT: Ge, Wangmao

APPLICANT: Geven B. Kanner

APPLICANT: Seven B. Kanner

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APPLICANT: Greven B. Kann
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APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
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APPLICANT: Now Profice Control of TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
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TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR PLILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-01-24
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Pred. No. 11;
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GIWGDSPEDIRKDLTFLGKDWGLEEMSEY 29
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SOFTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 262
LENGTH: 29
                                                                                                                                                                                    US-10-764-390-262
Sequence 262, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
APPLICANT: Agensy, Inc.
APPLICANT: Raitano, Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%;
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; ORGANISM: Homo sapiens
US-10-764-390-262
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CRGANISM: Homo sapiens
US-10-764-390-261
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US-10-764-390-261
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Sequence 43, Application US/10764390

Publication No. US20040214212A1

GENERAL INFORMATION:

APPLICANT: Raitano, Arthur B.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Ge, Wangmao

APPLICANT: Ferven B. Kanner

APPLICANT: Ferven B. Kanner

APPLICANT: GINVENTION: Entitled 254P1D6B Useful in Treatment and Detection of

TITLE OF INVENTION: Entitled 254P1D6B Useful in Treatment and Detection of

TITLE OF INVENTION: Canner

TITLE OF INVENTION: Canner

TITLE OF INVENTION: Canner

TITLE OF INVENTION: Canner

TITLE OF INVENTION: UNMBER: US60/442,526

PRIOR FILLING DATE: 2004-01-23

PRIOR FILLING DATE: 203-01-24

NUMBER OF SEQ ID NOS: 277

SOFTWARE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE FRASE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Butitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Daries 20081.00
CURRENT APPLICATION NUMBER: US(0/442,526
PRIOR PILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US(0/442,526
PRIOR PILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SSETWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                Sequence 267, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
148 WGLEEMSEYXDDYRELEKD 166
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                                                                                            1 WGLEEMSEYADDYRELEKD 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-764-390-43
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APPLICANT: Raitano, Arthur B.
APPLICANT: Taitano, Arthur B.
APPLICANT: Taitano, Arthur B.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Butiled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: UNMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR PILING DATE: 2004-01-23
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                              1.5%; Score 84; DB 16; Length 17; 94.1%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                  APPLICATIVE HYBERGY, INC.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILLE REFERENCE: 790CTB3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 52425
LENGTH: 19
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; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-52425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 83; DB 18; I
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                              ; Sequence 52425, Application US/10450763; Publication No. US20050196754A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 265, Application US/10764390, Publication No. US20040214212A1, GENERAL INFORMATION:
                                                                                                                                                                149 GLEEMSEYXDDYRELEK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAPPTGVLSSLLLLVTIA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Bid, Pia M.
                                                                                                                                                                                               1 GLEEMSEYADDYRELEK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                  Query Match
Best Local Similarity 94.1
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-390-260
                                                                                                                                                                                                                                                                    RESULT 8
US-10-450-763-52425
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APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REPERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT APPLICATION NUMBER: US/0/442,526
PRIOR APPLICATION NUMBER: US/0/442,526
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 260
LENGTH: 17
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                                                                 Gaps
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                     Query Match 1.6%; Score 92; DB 16; Length 16; Best Local Similarity 100.0%; Pred. No. 31; Matches 16; Conservative 0; Mismatches 0; Indels
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45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 260, Application US/10764390 Publication No. US20040214212A1 GENERAL INFORMATION:
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Best Local Similarity 94.1
Matches 16; Conservative
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ORGANISM: Homo sapiens
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Gaps ö

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TYPE: PRT
ORGANIEM: Artificial
PERTURES
OTHER INFORMATION: Synthetic Peptide
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US-10-682-103-3
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SEQ ID NO 1
LENGTH: 34
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Faris, Mar.
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
TITLE OF INVENTION: Builtied 254PlD6B Useful in Treatment and Detection of TITLE OF INVENTION: Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09892835

Publication No. US20020019016A1

FURBLIANT WINDOWNATION:

APPLICANT: Vanmechelen, Eugeen

APPLICANT: Vanderstichele, Huge

TITLE OF INVENTION: Differential Diagnosis of Neurological Diseases

FILE REFERENCE: INNS:027 (11362.0027.NPUS01)

CURRENT APPLICATION NUMBER: US/09/892.835

FRIOR APPLICATION NUMBER: US 09/892.835

PRIOR FILING DATE: 2001-06-27

PRIOR PILING DATE: 2001-06-27

PRIOR PELING DATE: 2000-07-18

PRIOR PLING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: EP 00870151.8

PRIOR PILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.2
                                                                                                                                                                              Gaps
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                                                                                                                                Length 24;
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100.0%; Pred. No. 1.7e+06;
trive 0; Mismatches 0; Indels
                                                                                                                                                                           0; Indels
                                                                                                                              Query Match
1.4%; Score 79; DB 16; I
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 51158-20081.00
CURRENT APPLICATION NUMBER: US/10/764,390
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US60/442,526
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOFTWARE: PastSEQ for Windows Version 4.0
SSOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                     Sequence 138, Application US/10764390
Publication No. US20040214212A1
GENERAL INFORMATION:
APPLICANT: Agensy, Inc.
APPLICANT: Raitano, Arthur B.
                                                                                                                                                                                                                                                             11 CARKOCSEGRIYSN 24
                                                                                                                                                                                                                    20 CARKOCSEGRIYSN 33
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Best Local Similarity 100.
Matches 9; Conservative
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                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-390-265
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                                                                                                                                                                                                                                                                                                                                                     -10-764-390-138
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  SEQ ID NO 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-892-835-1
                        LENGTH: 24
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176 PRGSABYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVL 235
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                                                                                                                                                                                                  Indels 37; Gaps
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                                                                                                                                       Query Match 1.1%; Score 61.5; DB 9; Length 34; Best Local Similarity 29.6%; Pred. No. 6.8e+03; Matches 21; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PRGAAP-----PGOKGOANAT-----RIPAKT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VanMechelen, Eugeen
APPLICANT: VanMechelen, Eugeen
TITLE OF INVENTION: Diagnosis of Tauopathies
FILE REFERENCE: US.112.T181
CURRENT APPLICATION NUMBER: US/09/769,180
CURRENT APPLICATION NUMBER: US/09/769,180
CURRENT APPLICATION NUMBER: EP 00870008.8
PRIOR APPLICATION NUMBER: EP 00870280.5
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/178,391
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 54
SOUTHWARE: Patentin version 3.0
NAME/KEY: MOD RES
LOCATION: (28)...(28)
COTHER INFORMATION: PHOSPHORYLATION THREONINE
US-09-892-835-1
                                                                                                                                                                                                                                                                                          ; LOCATION: (28)..(28); CTHER INFORMATION: PHOSPHORYLATION US-09-769-180-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09769180; Publication No. US20030194742A1; GENERAL INFORMATION:
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; Publication No. US20040091942A1
; GENERAL INFORMATION:
; APPLICANT: VanMechelen, Eugeen
                                                                                                                                                                                                                                                                                                                                                                         236 LPLPTTPSSGE 246
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FEATURE:
NAME/KEY: MOD RES
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1 EEMSEYSDDYRE 12
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CORGANISM: Homo sapiens
US-10-764-390-137
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APPLICANT: Agensys, Inc.
APPLICANT: Agensys, Inc.
APPLICANT: Asitano, Arthur B.
APPLICANT: Jakobovita, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Steven B. Kanner
APPLICANT: Juan J. Perez-Villar
APPLICANT: Juan J. Perez-Villar
APPLICANT: Juan J. Perez-Villar
APPLICANT: Juan J. Perez-Villar
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Kanner
APPLICANT: Steven B. Vander
GURENT FILING DATE: 2008-10.
CURRENT FILING DATE: 2004-01-23
FRIOR APPLICATION NUMBER: US60/442,526
FRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 277
SOPTWARE: FastSEQ for Windows Version 4.0
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29.6%; Pred. No. 6.8e+03;
tive 6; Mismatches 7; Indels 37
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APPLICANT: Vanderstichele, Hugo
TITLE OF INVENTION: Diagnosis of Tauopathies
FILE REFERENCE: 11916.0016.DVUS01 (INNSO16-1)
CURRENT APPLICATION NUMBER: US/10/682,103
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: 09/769,180
PRIOR APPLICATION NUMBER: EP 00870008.8
PRIOR APPLICATION NUMBER: EP 00870008.8
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VEREION 3.2
SEQ ID NO 3
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD RES
1 LOCATION: (28)
2 OTHER INFORMATION: PHOSPHORYLATION
US-10-682-103-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-764-390-41
; Sequence 41, Application US/10764390
; Publication No. US20040214212A1
; GENERAL INFORMATION:
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Best Local Similarity 29.69
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 LPLPTTPSSGE 246
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CRGANISM: Homo sapiens
US-10-764-390-41
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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151 EEMSEYXDDYRE 162

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APPLICANT: Rateano, Arthur B.
APPLICANT: Rateano, Arthur B.
APPLICANT: Rateano, Arthur B.
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Galilita-Eid, Fia M.
APPLICANT: Faris, Mary
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APPLICANT: Faris, Mary
APPLICANT: Bratish Galds and Corresponding Proteins
TITLE OF INVENTION: Butitled 254PlD6B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
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100.0%; Pred. No. 1.7e+06;
tive 0; Mismatches 0; Indels
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Sequence 137, Application US/10764390 Publication No. US20040214212A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-217-306B-19

US-09-338-315-54

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US-09-338-315-64

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Listing first 45 summaries
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length: 35
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APPLICANT: Vanmechelen, Eugeen
APPLICANT: Vanmechelen, Eugeen
APPLICANT: Vanmechelen, Eugeen
TITLE OF INVENTION: Differential Diagnosis of Neurological Diseases
FILE REFERENCE: INNS:027 (11362.0027.RPUS01)
CURRENT APPLICATION NUMBER: US /09/892,835
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/218.907
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: EP 00870151.8
PRIOR PRILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 1-06-30
NUMBER OF SEQ ID NOS: 1-06-30
SOFTWARE: Patentin version 3.2
IENGTH: 34
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US-08-35-456C-4
US-08-395-456C-4
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US-09-625-39A-15
US-09-636-399A-15
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LOCATION: (28)...(28)
OTHER INFORMATION: PHOSPHORYLATION THREONINE
US-09-892-835-1
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US-09-769-180-3
F Sequence 3, Application US/09769180
F Patent No. 6680173
GENERAL INFORMATION:
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Patent No. 6670137
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Query Match 1.1%; Score 59.5; DB 3; Length 35; Best Local Similarity 35.0%; Pred. No. 6.2e+02; Matches 14; Conservative 3; Mismatches 18; Indels
                INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                   , MOLECULE TYPE: peptide US-08-658-136-52
TELEFAX:
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APPLICANT: LANDES, GREGORY M
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: BOKKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
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Pred. No. 4.1e+02;
           APPLICANT: Vanderstichele, Hugo
TITLE OF INVENTION: Diagnosis of Tauopathies
FILE REPERENCE: US.112.7181
CURRENT APPLICATION NUMBER: US/09/769,180
CURRENT FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: EP 00870008.8
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
SPIOR FILING DATE: 2000-01-27
SOFTWARE OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
LENGTH: 34
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Best Local Similarity 29.6%; Pred. No. 4.1e
Matches 21; Conservative 6; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELECHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 52, Application US/08658136 Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MOD RES
LOCATION: (28)...(28)
COTHER INFORMATION: PHOSPHORYLATION
US-09-769-180-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 LPLPTTPSSGE 246
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                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
APPLICANT: VanMechelen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-658-136-52
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US-09-060-767B-4
; Sequence 4, Application US/09060767B
; Sequence 7020152
; GENERAL INFORMATION:
; APPLICANT: Well, Gary
APPLICANT: Chandrashekar, Ramaswamy
; TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Gaps
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                                                                                                                           1 VAYHWDFGDGSPG----QDTDEPRAEHSYLRPGDYRVQV 35
                                                                        560 VLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steven M. Ruben, et al.
TITLE OF INVENTION: 32 Human Secreted Proteins
FILE REPERENCE: P2006P1
CURRENT APPLICATION NUMBER: US/09/690,454
CURRENT FILING DATE: 2000-10-18
FRIOR PILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 60/044,039
PRIOR FILING DATE: MAY 30, 1997
PRIOR FILING DATE: MAY 30, 1997
PRIOR PILING DATE: MAY 30, 1997
PRIOR PILING DATE: MAY 30, 1997
PRIOR PLING DATE: MAY 30, 1997
PRIOR PILING DATE: MAY 30, 1997
PRIOR APPLICATION NUMBER: 60/048,190
PRIOR PILING DATE: MAY 30, 1997
PRIOR PILING DATE: MAY 30, 1997
PRIOR PILING DATE: MAY 30, 1997
PRIOR PILING DATE: MAY 30, 1997
PRIOR APPLICATION NUMBER: 60/056,296
PRIOR FILING DATE: MAY 30, 1997
PRIOR APPLICATION NUMBER: 60/056,296
PRIOR FILING DATE: MAY 30, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
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PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
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PRIOR PILING DATE: AUGUST 29, 1997
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PRIOR PILING DATE: AUGUST 29, 1997
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PRIOR PILING DATE: AUGUST 29, 1997
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PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
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PRIOR PILING DATE: AUGUST 29, 1997
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PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                  US-09-690-454-177
; Sequence 177, Application US/09690454
; Patent No. 6531447
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US-09-690-454-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hassan, Helle
APPLICANT: Clausen, Henrik
APPLICANT: Clausen, Henrik
APPLICANT: Bennett, Eric P.
TITLE OF INVENTION: Glycosylation Using GalNAc-T4 Transferase
FILE REFERENCE: 8850*1
CURRENT APPLICATION NUMBER: US/09/217,306B
CURRENT FILIGO DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%; Score 53.5; DB 4; Length 24; Best Local Similarity 50.0%; Pred. No. 1e+03; Matches 11; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                            Query Match 1.0%; Score 54; DB 4; Length 25; Best Local Similarity 45.8%; Pred. No. 9.8e+02; Matches 11; Conservative 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SPARKS, Andrew B.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: OILLIAM, Lawrence A.
APPLICANT: POWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIBER, James B.
TITLE OF INVENTION: ISOLATING AND USING SAME
TITLE OF INVENTION: H. capsulatum
FILE REPERENCE: BJCH 9986
CURRENT APPLICATION NUMBER: US/09/060,767B
CURRENT FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/043,332
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                            291 PVLTVTPGSTEHSIPTPPTSAAPS 314
                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Caldocellum saccharolyticum
US-09-060-767B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 prstvrprprprprprprvrarpr 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54, Application US/08602999A Patent No. 6184205
GENERAL INFORMATION:
GAPPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/09217306B Patent No. 6465220 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 TPSAT---TPAPPSSSAPPETT 22
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC FEATURE
OTHER INFORMATION: Muc7
US-09-217-306B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-217-306B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-602-999A-54
                                                                                                                                                                                    SEQ ID NO 4
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 19
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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Gaps
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APPLICANT: KAY, BRIAN K.
APPLICANT: THORN, JUDITH M.
APPLICANT: THORN, JUDITH M.
APPLICANT: OLILLIAM, LARRENCE A.
APPLICANT: OLILLIAM, LARRENCE A.
APPLICANT: OLINGANINON: SIC SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1755 S. Jefferson Davis Highway, Suite 400 STATE: Virainis
STATE: New York
CUUNTRY: U.S.A.
ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: A35
ATTORNEY/AGENT INFRWATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 1101-202
TELEFHONE: (212) 790-9090
TELEFRONE: (212) 790-9041/8864
TELEFRONE: (212) 869-9741/8864
TELEFRONE: GA41 PERNIE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTER.STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 3; 3
Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4980-007-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22202
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 54, Application US/08278865
Patent No. 6303574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REFEISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 SESTPSELPISPTTAP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 ŚRŚTPRPLPMLPTTRP 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-602-999A-54
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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                    314 SESTPSELPISPITAP 329
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                                                             14 SRSTPRPLPMLPTTRP 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
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                                                                                                                                                                                                                                         Query Match 0.9%; Score 51; DB 3; Length 31; Best Local Similarity 62.5%; Pred. No. 2.4e+03; Matches 10; Conservative 1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: STARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: OUILLIAM, Lawrence A.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, Channing J.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: 150LATING AND USING SAME
NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 450

NUMBER OF SEQUENCES: 450

CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonde
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
CUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTONNEY/AGENT THORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECHONE: (212) 790-9090;
TELEPHONE: (212) 869-9741/8864
TELEPAX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54, Application US/09500124
Patent No. 6432920
                                                                                                                                                                                                                                                                                                                                314 SESTPSELPISPITAP 329
(703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                           14 SRŠTPRPLPMLPTRP 29
                TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEG ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                  MOLECULE TYPE: peptide US-08-278-865-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-09-500-124-54
                                                                                                                                                       unknown
                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
TELEPHONE:
                                                                                                                                                    TOPOLOGY:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                           STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRING DATE: 23-Aug-2001

CLASSIFICATION NOWBER: US/09/938,315

FILING DATE: 23-Aug-2001

CLASSIFICATION: CUNKNOWN>

ATTORNEY/AGRY INFORMATION:

NAME: Villacorta, Gilberto M.

REFERENCE/DOCKET NUMBER: 34,038

REFERENCE/DOCKET NUMBER: 4980-007-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-430-564-9

Sequence 9, Application US/09430564

Patent No. 6372467

GENERAL INFORMATION:
APPLICANT: John Blenis
APPLICANT: Kay K. Lee-Fruman
APPLICANT: Calvin J. Kuo
TITLE OF INVENTION: P5486K AND P8556K GENES, PROTEINS,
TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
FILE REFERENCE: 00246/506002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 0.9%; Score 51; DB 4; Length 31; Best Local Similarity 62.5%; Pred. No. 2.4e+03; Matches 10; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-938-315-54
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US-09-223-043-6

Sequence 6, Application US/09223043

Sequence 6, Application US/09223043

Father No. 617728-6

GENERAL INFORMATION:

APPLICANT: McKenzie, Ian F.C.

APPLICANT: Pieterz, Geoff A.

TITLE OF INVENTION: ANTIGENIC CARBOHYDRATE COMPOUNDS AND TITLE OF INVENTION: THEIR USE IN IMMUNOTHERAPY

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann Dorfman Herrell and Skillman

STREET: Suite 720, 1601 Market Street

CITY: Philadelphia

STREET: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 23;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,807
FILING DATE:
CLACKTEATO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/223,043
                                                                                                                                                                                                                                              FILING MAILS

CLASSIFICATION: 424

PRIOR APPLICATION DATH:
APPLICATION UNDER: US 08/340,711

FILING DATE: 16-NOV-1994

APPLICATION NUMBER: AU PM3223

FILING DATE: 24-DEC-1993

ATTORNEY AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643

REGISTRATION NUMBER: 27,643

REGISTRATION NUMBER: 23,647/PAS/MKR

TELEPHONE: (215)563-4100

TELEPHONE: (215)563-4044

INFORMATION POR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 mains acids
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REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 530547/PAS/MKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Pennsylvania
COUNTRY: United States of America
ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 TVTPGSTEHSIPTPPTSAAPSE 315
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: AU PM3223
FILING DATE: 24-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
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| Sequence 15, Application US/09430564
| Patent No. 6372677
| GENERAL INFORMATION:
| APPLICANT: Asy K. Lee-Fruman
| APPLICANT: Calvin J. Kue Pruman
| TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
| TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
| TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
| CURRENT FILING DATE: 1999-10-29
| PRIOR APPLICATION NUMBER: 60/106,141
| PRIOR FILING DATE: 1999-10-29
| WUMBER OF SEQ ID NOS: 16
| SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08833807
; Patent No. 5989552
; GENERAL INPORMATION:
    APPLICANT: McKenzie, Ian F.C.
    APPLICANT: Apostolopoulos, Vasso
    APPLICANT: Apostolopoulos, Vasso
    APPLICANT: Apostolopoulos, Vasso
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    APPL
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                                                         CURRENT APPLICATION NUMBER: US/09/430,564
CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/106,141
PRIOR FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 22
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COUNTRY: United States of America
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ORGANISM: Homo sapiens
US-09-430-564-15
                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-564-9
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Best Local Similarity
Matches 10; Conserva
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LENGTH: 22
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; Sequence 6, Application US/09593870A
; Patent No. 6548643
; GENERAL INFORMATION:
; APPLICANT: McKenzie, lan F.C.
; APPLICANT: Pietersz, Geoff Allan
; TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
; TITLE OF INVENTION: Use in Immunotherapy
; FILE REFERENCE: 2368-McKenzie
; CURRENT APPLICANTION NUMBER: US/09/593,870A
; CURRENT FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-593-870A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9%; Score 49; DB 4; Length 23; Best Local Similarity 40.9%; Pred. No. 2.2e+03; Matches 9; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                 Query Match 0.9%; Score 49; DB 3; Length 23; Best Local Similarity 40.9%; Pred. No. 2.2e+03; Matches 9; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         294 TVTPGSTEHSIPTPPTSAAPSE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TAAPPTPPATTPAPPSSSAPPE 23
; TELECOMMUNICATION INFORMATION:
; TELEPAX: (215)563-4100
; TELEPAX: (215)563-4100
; TELEPAX: (215)563-4044
; INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: 6: LENGTH: 23 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: DFOLOGY: linear
; MOLECULE TYPE: peptide
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Search completed: October 12, 2005, 10:31:46 Job time : 27 secs

294 TVTPGSTEHSIPTPPTSAAPSE 315

2 TAAPPTPATTPAPPSSSAPPE 23

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

October 12, 2005, 10:25:25; Run on:

; Search time 67 Seconds (without alignments) 8193.267 Million cell updates/sec

US-10-764-390-3 5580

1 MAPPTGVLSSLLLLVTIAGC.....VSMNGSIRNGASFSYCSKDR 1072 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 35

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q7m4e6 drosophila	Q6pjk3 homo sapien	Q8clu0 yersinia pe	P61104 ornithocton	P01535 anemonia su	Q61d14 homo sapien						Q70222 human immun	Q9ymb1 human immun				_	Q735g0 bacillus ce	Q80586 human immun	Q8j3x2 human immun	P01498 androctonus	Q8ixg1 homo sapien		Q74en3 geobacter s	085607 streptomyce	Q38675 bacteriopha			•	Q9zg81 chlamydia t	Q83333 murine hepa
OI	Q7M4E6	Q6PJK3	OBCLUO	TXH5 ORNHU	TXA3 ANESU	Q6LD14	Q8WLR1	SCK1_TITCA	Q7YP58	Q6WY52	TAT_SIVM2	Q70 <u>2</u> 22	Q9YMB1	Q9Y181	Q7R7E1	Q87JB9	039816	Q735G0	080586	Q8J3X2	SCXP ANDMA	QBIXGI	Q8EFK7	Q74EN3	085607	Q38675	Q77D54	Q9AZ16	Q7Y043	Q9ZG81	083333
08	~	N	7	ч	ч	~	0	ч	~	~	-	~	~	N	~	~	N	N	N	~	-	~	~	~	7	~	~	~	~	N	0
Length	32	34	27	32	27	18	21	23	24	59	32	34	32	27	53	33	33	34	32		32		33	32	22	56	26	27	34	34	35
% Query Match	6.0	0.9	6.0	6.0	6.0	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8		•	0.8	0.8	0.8	0.8	•	9.0	0.8	•	•	0.8	0.8
Score	51	48.5	48	48	47.5	47	47	47	46	46	46	46	45.5	45	45	45	45	44.5	44.5	44	44	43.5	43.5	•	43	43	43	43	43	43	43
Result No.	-	64	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	58	53	30	31

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE=Brain,

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.D., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleh F.,

Diatchenko L., Marusina X., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

ALIGNMENTS

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Hernandez G., Sierra J.M.;
"Translation initiation factor eIF-4E from Drosophila: cDNA sequence and expression of the gene.";
Biochim. Biophys. Acta 1261:427-431(1995).
DIR, S55937; S55937.
NON TER 32 32
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                           ö
               01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
17-maislation initiation factor elf-4E (Fragments).
Drosophila melanogaster (Fruit fly).
Enkaryota; Metazoa; Arthropods; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroides; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                              Length 32;
                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                 32 AA; 3364 MW; C492C82B551A6959 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                            / Match 0.9%; Score 51; DB 2;
Local Similarity 68.8%; Pred. No. 3e+04;
Nes 11; Conservative 0; Mismatches
32 AA.
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 PRT;
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PRELIMINARY;
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 Q7M4E6
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Matches
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Toxicon 42:15-20(2003).

-i-FUNCTION: HwTx-V reversibly paralyzes locusts and cockroaches, and causes death with larger doses. It has no effect on mice by intra-abdominal, nor intracerebrowenticular injection. Its natural mutant mHwTx-V shows no effect on locusts, cockroachs, and mice.
-i-SUBCELLULAR LOCATION: Secreted.
-i-TISSUE SPECIFICITY: Expressed by the venom gland.
-i-MASS SPECIFICITY: MW-4111.4; MW_ERR=0.4; METHOD=MALDI; RANGE=1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- MASS SPECTROMETRY: MW=3877.1; MW_ERR=0.4; METHOD=MALDI; RANGE=1-
      05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annocation update)
Huwentoxin-V (HWTX-V) [Contains: Mutant of huwentoxin-V (mHWTX-V)].
Ornithoctomus huwena (Chinsse bird spider) (Selenocosmia huwena).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Ornithoctonus.
                                                                                                                                                                                                                                                            Zhang P.-F., Chen P., Hu W.-J., Liang S.-P.; and the spider Huwentoxian-V, a novel insecticidal peptide toxin from the spider Selenaccemia huwena, and a natural mutant of the toxin: indicates key amino acid residues related to the biological activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Chidoblast,
MEDLINE=78084776; PubMed=23311; DOI=10.1016/0014-5793(77)80699-6;
Martinez G., Kopeyan C., Schweitz H., Lazdunski M.;
"Toxin III from Anemonia gulcata: primary structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; NOTE=Ref.1.
-!- MISCELLANEOUS: ED(50) of HwTx-V is 16 +/- 5 mg/kg to locusts.
Direct protein sequencing; Neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neurotoxin III (Toxin ATX-III).
Anemonia sulcata (Snake-locks sea anemone).
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=7804477; PubMed=21843;
Beress L., Wunderer G., Wachter E.;
"Amino acid sequence of toxin III from Anemonia sulcata.";
Hoppe-Seyler's Z. Physiol. Chem. 358:985-988(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              By similarity.
By similarity.
By similarity.
CC39F421571CA523 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huwentoxin-V. Mutant of huwentoxin-V.
                                                                                                                                                                                                                                        PubMed=12893056; DOI=10.1016/S0041-0101(03)00095-3;
                                                                                                                                                                                               SEQUENCE, DISULFIDE BONDS, AND MASS SPECTROMETRY. TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . No. 4.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         917 CSGHGHCDPLTKRCICSHLWMENLIQRYIWDG 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 CSQDGDC----CXHLQCHSNYEWCVWDG 32
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MEDLINE=93343891; PubMed=8102051;
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                                                                                                                                                          NCBI_TaxID=29017;
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.B., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Hellon E.K., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
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DOI=10.1128/JB.184.16.4601-4611.2002;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry R.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Indels
                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 184;4601-4611(2002).
EMBL, AE013624; AAM813835.1; -
HYPOCHACICAL protein.
SEQUENCE 27 AA; 3211 MW; A5203621B3DE0ABC CRC64;
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7B38FEFC8B7809D4 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best Local Similarity 39.1%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC014386; AAH14386.2;
                                                                                                                                                                                                                                                                                                                                                                                                                               34 AA; 3886 MW;
                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
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35 AA.

PRT;

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RESULT 4

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Gaps

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Length 35; Indels 21 AA.

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PRELIMINARY;
  CCCCCSVQKR 18
                                                                                                                                             Homo sapiens (Human)
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P83243;
                                                                                                                                    Name=HLA-B;
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SEQUENCE
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Best Local S
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Ionic channel inhibitor, Neurotoxin, Sodium channel inhibitor, Toxin.
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                 Manoleras N., Norton R.S.;
"Three-dimensional structure in solution of neurotoxin III from the sea anemone Anemonia sulcata.";
slockhemistry 33:11051-11051(1994).
-!- FUNCTION: Binds specifically to the sodium channel.
-!- SUBCELLULAR LOCATION: Secreted; cnidocyst.
-!- SIMILARITY: Belongs to the sea anemone short toxin family.
PDB; A94446; TZAZ3.
Norton R.S., Cross K., Braach-Maksvytis V., Wachter E.; "IH-NMR study of the solution properties and secondary structure of neurotoxin III from the sea anemone Anemonia sulcata.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE PROM N.A.

MEDLINE=95038742; Pubmed=7951233;

Haire R.N., Ohta Y., Lewis J.E., Fu S.M., Kroisel P., Litman G.W.;

Haire R.N., Ohta Yroisel bushe kinase expressed in T cells shares sequence identity with Tec family kinases and maps to 4pl2.";

Hum. Mol. Genet. 3:897-901(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
                                                                                                                                                                                                                                                                                                                                  7; Indels 13;
                                                                                                                                                                                                                                                                                                          0.9%; Score 47.5; DB 1; Length 27; 28.1%; Pred. No. 3.6e+04; ive 3; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 2; Length 18; Pred. No. 2.2e+04; O; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL, U07791, AAA19597.1; -.
GO, GO:0016301, F:kinase activity, IEA.
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22
23 CS -> SC (in Ref. 2).
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2938 MW; AA4E261FFAF34A7A CRC64;
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18 18
18 AA; 2025 MW; D954E7BB497625B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                             60 ACCDLSSCDLAWWFEGRCYLVSCPHKENCEPK 91
                                                                                                                                                                                                                                                                                                                                                                           2 SCCP-----CYWGGCPWGQNCYPE 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                        PubMed=7727358;
                                      Biochem. J. 293:545-551(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.8%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyrosine kinase (Fragment)
                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Peripheral blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    27 AA;
                                                             STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                           Ionic channel
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6LD14
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STRUCTURE BY NMR.
PubMed=11790849; DOT=10.1110/ps.33402;
Wang I., Wu S.H., Chang H.K., Shieh R.C., Yu H.M., Chen C.;
"Solution structure of a K(+)-channel blocker from the scorpion Tityus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20565534; PubMed=11113450; DOI=10.1016/S0014-5793(00)02253-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Batista C.V.F., Gomez-Lagunas F., Lucas S., Possani L.D.; "TC1, from Tityus cambridgei, is the first member of a new subfamily of scorpion toxin that blocks K(+)-channels."; FEBS Lett. 486:117-120(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chelicerata; Arachnida; Scorpiones;
                                                                                                                                                                                                                                                                                Vargas-Alarcon G., Gomez-Casado B., Martinez-Laso J., Granados J.,
Lystisse Z., Alegre R., Arnaiz-Villona A.,
"Differences in intron 2 sequences between B*39061 and B*39062 in
Amerindians: comparison with those of B*3901, B*5101, and B*52012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cambridgei.";
Protein Sci. 11:390-400(2002).
-!- FUNCTION: Blocks reversibly Shaker B potassium channels. Also
displaces binding of noxiustoxin to mouse brain synaptosome
                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                             TISSUE=Blood;
MEDLINE=97246738; PubMed=9089103; DOI=10.1007/s002510050227;

    -!- SUBCELLULAR LOCATION: Secreted.
    -!- TISSUB SPECIFICITY: Expressed by the venom gland.
    -!- MASS SPECTROMETRY: MW=2446.4; METHOD=MALDI; RANGE=1-23;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AA; 1972 MW; 5941EC53ECF3A73D CRC64;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Major histocompatibility complex class I (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 2; 1
Pred. No. 2.7e+04;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Tityus cambridgei (Amazonian scorpion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Arthropoda, Cheli.
Buthida, Buthoidea, Buthidae, Tityus.
                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 45:436-439(1997).
EMBL; L77205; AAL40076.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 NRPPAALGGSGPDRDL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                622 NRPPVAV - AGPOKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 56.2
9; Conservative
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Gaps

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Length 29; Indels

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE STATEMENT TRANSCRIPTIONAL REGULATOR THAT ACTS BY binding to the trans-activating responsive sequence (TAR) RNA element and activates transcription initiation and/or elongation from the LTR
                Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
"Experimented evolution yields hundreds of mutations in a functional voiral genome.";
J. Mol. Evol. 57:241-248(2003).
EMBL; AXZ64777; AAB74429.1;
EMBL; AXZ64777; AAB740.1;
SEQUENCE 29 AA; 3217 MW; SEF0F978F980B9D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=88122665; PubMed=2893293; DOI=10.1038/331619a0;
Kestlar H.W., Li Y., Naidu Y.M., Butler C.V., Ochs M.F., Jaenel G.,
King N.W., Daniel M.D., Desrosiers R.C.;
"Comparison of simian immunodeficiency virus isolates.";
Nature 331:619-622(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAT protein (Transactivating regulatory protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.8%; Score 46; DB 1; Length 32; 42.1%; Pred. No. 5.3e+04; vative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simian immunodeficiency virus (Mm251 isolate) (SIV-MAC).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 AA; 3556 MW; 211547CBE6F4D817 CRC64;
                                                                                                                                                                           0.8%; Score 46; DB 2; Le. ilarity 47.1%; Pred. No. 4.7e+04; Conservative 3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, X06879; -; NOT ANNOTATED_CDS.
HIV; X06879; TAT$MM251.
Activator; AIDS; Nuclear protein; RNA-binding;
Transcription regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                        32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 AA
MEDLINE=22990536; PubMed=14629033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 PEKAKKETVEKAVATAPGL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 09, Created)
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                                                                                                                                                                                                Local Similarity
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01-NOV-1988 (
05-JUL-2004 (
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8
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ID TAT_SIVM2
AC P05912;
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SEQUENCE
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ID Q70222
AC Q70222;
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Matches
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            -!- SIMILARITY: Belongs to the short scorpion toxin family. Potassium channel inhibitor subfamily. PDB; 1JLZ; NWR; A=1-23.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                 Interaction with Ca(2+)-activated K(+)
                                                                   GO; GO:0005576; C:extracellular; NAS.
GO; GO:0019875; E:potassium channel inhibitor activity; IDA.
GO; GO:0019835; P:cytodygis; IDA.
GO; GO:0009405; P:pathogenesis; IDA.
Interpro; IPR001947; Scorpion toxins.
BNGSITE; PS01138; SCORP SHORT TOXIN; FALSE NEG.
3D-structure; Direct protein sequencing; Ionic channel inhibitor;
Neurotoxin; Potassium channel inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                          5
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8%; Score 47; DB 1; Length 23; Best Local Similarity 45.0%; Pred. No. 3.1e+04; Matches 9; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 56.2%; Score 46; DB 2; Length 24; Similarity 56.2%; Pred. No. 3.6e+04; 9; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bendukidze N.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                        channels (Potential).
D59BFADBC9F31700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AA; 2337 MW; 2AAEA853EC8BD316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPES,
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I antigen (Fragment).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                913 CLLKCSGHGHCDPLTKRCIC 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRKKCKGSGKC--INGRCKC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ579377; CAE18166.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              622 NRPPVAVA--GPDKEL 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||||:|
7 NRPPAALGSPGPDRDL 22
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                                                                                                                                                                                                                                                                                                                                           2454 MW;
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Matches 9, Conserv
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SEQUENCE
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Q6WY52
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10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 Priapulus caudatus.
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=37621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=PY07646;
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SEQUENCE
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     Matches
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                                                                                                                                                                                                                                                                 MEDLINE=95074931; PubMed=7527089;
Mammano F., Salvatori F., Ometto L., Panozzo M., Chieco-Bianchi L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Virol. 144:29-43(1999).

EMBL; ABO1146; BAA75967.1; -

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral capaid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; F:structural molecule activity; IEA.

InterPro; IRR00777; GP120.

Pfam; PF00516; GP120; 1.

AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                "Relationship between the V3 loop and the phenotypes of human immunodeficiency virus type 1 (HIV-1) isolates from children immunodeficiency virus type 1 (HIV-1) isolates from children perinatally infected with HIV-1.";

J. Virol. 69.82-92(1995).

EMBL; U10001; AAA64813.1; -...

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral enyelope; IEA.

GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 2; Length 34;
Pred. No. 5.8e+04;
5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 TLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGH 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TRPNNNTRRSIHIGPGRAF-----YPTDIIGDIRQAH 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 AA; 3851 MW; BB88F3A44AAAE0EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35F41F3CE68499DF CRC64;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein v3 loop region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                      Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-JUN-2003 (TrEMBLrel. 24, Last a
Envelope glycoprotein (Fragment).
                                                                                                                  Human immunodeficiency virus 1.
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3878 MW;
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Best Local Similarity
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35 AA;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Stelengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., R., Redmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 0:0-0(1999).

Nature 0:0-0(1999).

-1 - SUBCELULAR LOCATION: Nuclear (By similarity).

EMBL; AF144895; AAD40651.1; -.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001356; Homeobox.

InterPro; IPR009057; Homeodomain_like.

PRNTNS; PR00124; HOMEOBOX.

PROSITE; PSS0011; HOMEOBOX.

DNA-binding; Homeobox; Nuclear protein.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
346 TLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGH 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 2; Length 27; Pred. No. 4.7e+04; 4; Mismatches 5; Indels
                       2 TRPNNNTRKGVYIGPG-----RAVFYATDIIGDIRQAH 34
                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Priapulida; Priapulidae; Priapulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 AA; 3288 MW; 321AE16A0529F351 CRC64;
                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2004 (TrEMBLrel. 26, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 AA.
                                                                                                                                                    27 AA
                                                                                                                                                                                                                                                                       Engrailed homeodomain protein (Fragment).
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                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.00,
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Carucci D.J.;
"Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelli yoelli.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is Parliminary data.

EMBL/ABLO1002846; EAA20148.1; -.
Hypothetical protein.
NON TER
                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                           Query Match 0.8%; Score 45; DB 2; Length 29; Best Local Similarity 36.0%; Pred. No. 5.2e+04; Matches 9; Conservative 6; Mismatches 10; Indels
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Search completed: October 12, 2005, 10:30:37 Job time : 69 BECB

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 12, 2005, 10:26:00 ; Search time 21 Seconds (without alignments) 4911.637 Million cell updates/sec

US-10-764-390-3 5580 Perfect score: Sequence:

1 MAPPIGVLSSLLLLVTIAGC......VSMNGSIRNGASFSYCSKDR 1072

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

7756 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 35 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	translation initia	cenA protein (IgA1	POU homeodomain pr	toxin III - snake-	tubulin alpha chai	neurotoxin P2 - sc	isocitrate dehydro	metallothionein -	gene 1.5 protein -	hypothetical prote		hypothetical prote			retinoic acid rece	coenzyme F420 hydr	T-cell receptor va	neural cell adhesi	gamma-crystallin -	major immunophilin		gurmarin - Gymnema	ATP synthase beta-	ribosomal protein	cysteine proteinas	retinoic acid rece	Ig heavy chain CDR	pollen allergen Po	tyrosine 3-monooxy
SUMMARIES		S55937	140692	B49111	TZAZ3	C56635	NTSRPM	S58433	SMMR	Q1BP57	F95172	C83797	D84404	T29628	G97596	167427	S63483	D49829	G39690	S12965	C49480	153186	JX0200	A48186	808569	A44912	167428	PT0286	A60372	PN0583
	DB	~	~	~	Н	~	Н	~	-	Н	~	N	N	N	N	~	7	~	0	7	7	N	~	7	~	N	~	0	~	7
	Query Match Length	32	25	25	27	34	35	22	25	29	35	28	31	31	31	34	20	28	29	30	32	33	35	23	28	30	34	18	20	27
de	Query Match	0.9	6.0	6.0	6.0	0.8	0.8	0.8	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7
	Score	51	50.5	49	47.5	44	44	42	41	41	41	40.5	40.5	40.5	40.5	40.5	40	40	40	40	40	40	40	φ.	6.	6	6		39	
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hypothetical 3.1K chymotrypsin (EC 3	hypothetical prote photogystem I 14.4 group I allergen A	neurotoxin BmK 41- group I allergen P group I allergen A	aspartate transcar hemoglobin AIV'- hypothetical prote	hypothetical prote V3 domain peptide alwhalmlingodidee	capsid protein VP1 45/47K antigen - M
JS0676 A61529	B85840 PQ0672 B58493	A59356 E58493 F58493	S51176 S01811 G84147	C82520 PC2297	321240 PQ0545 A49237
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30 31	64 64 44	35 36 37	3 8 8 9 0 0	441	4 4 4 J 4 7

ALIGNMENTS

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Cyaccesion: S55937

R. Hernandez, G.; Sierra, J.M.

Biochim. Blophys. Acta 1261, 427-431, 1995

A; Pittle: Translation initiation factor eIF-4E from Drosophila: cDNA sequence and express A; Reference number: S55936; MUID:95260867; PMID:7742371

A; Accession: S55337

A; Status: preliminary

A; Residues: 1-8,9-27;28-32 - HER->
A; Conserreferences: UNIPROT:Q7M4E6

C; Genetics:
translation initiation factor eIF-4B - fruit fly (Drosophila melanogaster) (fragments) C,Species: Drosophila melanogaster C,Species: 27-0ct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross references: FlyBase: FBgn0013947
C; Superfamily: translation initiation factor eIF-4E
                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Gene: FlyBase: Eif4F
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299 STEHSIPTPPTSAAPS 314 13 ŚrEQGRPEPPTSAAAS 28 g ઠે

CenA protein (IgAlh) - Cellulomonas fimi (fragment)
C;Species Cellululomonas fimi
C;Species Cellululomonas fimi
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C;Accession: I40692
E;Accession: I40692
E;Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warren FEMS Microbiol. Lett. 92, 199-204, 1992
A;Pitle: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human IgA

A,Residues: 1-25 <RES> A,Crose-references: EMBL:X65780; NID:g312035; PIDN:CAA46663.1; PID:g312036 A;Reference number: 140692
A;Accession: 140692
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

Gарв 6 Query Match

0.9%; Score 50.5; DB 2; Length 25;
Best Local Similarity 48.1%; Pred. No. 3e+03;
Matches 13; Conservative 2; Mismatches 3; Indels

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303 SIPTPPTSAAPSESTPSELPISPTTAP 329

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Gaps ö

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RiRosso, J.P.; Rochat, H.
Toxicon 23, 113-125, 1985
Tyritle: Characterization of ten proteins from the venom of the Moroccan scorpion Androc A; Reference number: A94318; WUID:85193276; PMID:3992595
A;Accession: A01758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isocitrate dehydrogenase (NAD) (EC 1.1.1.41) chain 2 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: S58433
R;Zeng, Y.; Weiss, C.; Yao, T.T.; Huang, J.; Siconolfi-Baez, L.; Hsu, P.; Rushbrook, J.1
B;chem. J. 310, 507-516, 1995
A;Title: Isocitrate dehydrogenase from bovine heart: primary structure of subunit 3/4.
A;Reference number: S58432; MUID:95382766; PMID:7654189
                                                                                                                                              A;Note: sequence extracted from NCBI backbone (NCBIN:128392, NCBIP:128391)
C;Superfamily: tubulin
F;28/Andring site: polyglutamate (Glu) (covalent) #status predicted
F;33-34/Cleavage site: Glu-Tyr (tubulin-specific carboxypeptidase) #status predicted
F;33-34/Cross-link: peptide (Glu-Tyr) (by tubulin-tyrosine ligase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Androctonus mauretanicus mauretanicus C;Date: 15-Oct-1982 #sequence_revision 15-Oct-1982 #text_change 09-Jul-2004 C;Accession: A01758
                                                                                                                                                                                                                                                                                                                                       Ouery Match 0.8%; Score 44; DB 2; Length 34; Best Local Similarity 32.0%; Pred. No. 1e+04; Matches 8; Conservative 7; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: scorpion neurotoxin
C;Keywords: neurotoxin; venom
F;1-18,4-25,15-30,19-32/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 1; I
Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurotoxin P2 - scorpion (Androctonus mauretanicus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nilarity 30.4%; Pred. No. 1.1e
Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:Q7M3F1
C;Superfamily: 3-isopropylmalate dehydrogenase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 EEMSEYXDDYRELEKDLLQPSGKQE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 EDMAALEKDYEEVGVDSIEGEGEEE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            913 CLLKCSGHGHCDPLTKRCICSHL 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 CATCGGGRGKC--VGPQCLCNRI 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPROT: P01498
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Best Local Similarity
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A;Molecule type: protein
A;Residues: 1-22 <ZEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 1-35 < ROS>
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Matches 7, Conserv
                                A,Accession: C56635
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-34 <COE>
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                                                                                                                                                                           C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: B9111
R:Das. G.; Herr, W.
J. Biol. Chem. 268, 25026-25032, 1993
A:Title: Enhanced activation of the human histone H2B promoter by an Oct-1 variant gener A;Reference number: A49111; MUID:94043371; PMID:8227066
A;Contents: NTera 2D1
A;Accession: B49111
A;Accession: B49111
A;Accession: B49111
A;Accession: compared with conceptual translation
A;Wolecule type: nucleic acid
A;Residues: 1-25 cDAS>
A;Note: sequence extracted from NCBI backbone (NCBIP:139679)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Oncorhynchus keta (chum salmon)
C;Species: Jl-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 10-Jul-1998
C;Accession: C56635
R;Coe, I.R.; Munro, R.; Sherwood, N.M.
B,Coe, I.R.; Munro, R.; Sherwood, N.M.
A;Title: Isolation of different brain-specific isotypes of alpha-tubulins from chum salm A;Reference number: A56635; MUID:93208376; PMID:1296820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tubulin alpha chain, brain-specific isotype (clone pTUB6) - chum salmon (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toxin III - snake-locks sea anemone
C;Species: Anemonia sulcata (snake-locks sea anemone)
C;Species: Anemonia sulcata (snake-locks sea anemone)
C;Date: 30-Apr-1979 #sequence revision 24-Sep-1981 #text_change 09-Jul-2004
C;Accession: A91446; A91674; A01798
R;Martinez, G.; Kopeyan, C.; Schweitz, H.; Lazdunski, M.
FRES Lett. 84, 24-252, 1977
A;Title: Toxin III from Anemonia sulcata: primary structure.
A;Reference number: A91446; MUD: 78084776; PMID: 23311
A;Residues: 1-27 < MAR>
A;Residues: 1-27 < MAR>
A;Residues: 1-27 < MAR>
A;Residues: J.; Wunderer, G.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 358, 985-988, 1977
A;Title: Amino acid sequence of toxin III from Anemonia sulcata.
A;Reference number: A91674; MUD: 78044787; PMID: 21843
A;Accession: A91674
A;Molecule type: protein
A;Residues: 1-21, SC', 24-27 < C;Comment: Three disulfide bonds are present.
C;Superfamily: toxin III
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28.1%; Pred. No. 4.9e+03;
tive 3; Mismatches 7;
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Matches 9; Conserv
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CiSpecies: Streptococcus preumoniae
CiSpecies: Streptococcus preumoniae
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CiDate: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
CiAccession: F95172
R;Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Reference number: A95000; MUD:21357209; PMID:11463916
A;Accession: F95172
A;Accession: Fpellminary
A;Retailuser: DNA
A;Residues: 1-35 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q97PV9; GB:AE005672; PIDN:AAK75575.1; PID:g14972972; GSPDB:G
A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
R;Takami, H:; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira.
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
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A;Experimental source: strain C-125
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C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: D64404
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. P.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Danniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
hypothetical protein SP1481 [imported] - Streptococcus pneumoniae (strain TIGR4)
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Pred. No. 1.6e+04;
4; Mismatches 7; Indels
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Pred. No. 1.2e+04;
5; Mismatches 7;
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Best Local Similarity 38.1%;
Matches 8; Conservative
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Best Local Similarity 42.1%;
Matches 8; Conservative
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A; Residues: 1-28 <STO>
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                    metallothionein - cultivated mushroom
C;Species: Agaricus bisporus (cultivated mushroom)
C;Species: Agaricus bisporus (cultivated mushroom)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A03286
R;Munger, K.; Lerch, K.
Biochemistry 24, 675-1-6756, 1985
A;Title: Copper metallothionein from the fungus Agaricus bisporus: chemical and spectros
A;Reference number: A03286
A;Attle: Copper protein
A;Residues: 1-25 < AUM)
A;Ccoss-references: UNIPROT:P04358
A;Cross-references: UNIPROT:P04358
A;Cross-references: UNIPROT:P04358
C;Comment: In contrast to the vertebrate metallothioneins, the fungal proteins bind copp
C;Comment: The absorptive, luminescent, and stereoptical properties of the copper MT are
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster
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Local Similarity 41.2%; Pred. No. 9.7e+03;
les 7; Conservative 2; Mismatches 8;
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A; Accession: D84404

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C;Species: Rattus porvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 167427
R;Lopes da Silva, S.; Van Horssen, A.M.; Chang, C.; Burbach, J.P.
Endocrinology 136, 2276-2283, 1995
A;Title: Expression of nuclear hormone receptors in the rat supraoptic nucleus.
A;Reference number: 153294; MUID:95237162; PMID:7720676
A;Reference number: 153294; MUID:95237162; PMID:7720676
A;Reference number: 153294; MUID:95237162; PMID:7720676
A;Reference number: 153294; MUID:95237162; PMID:7720676
A;Reference number: 153294; MUID:95237162; PMID:7720676
A;Redidues: 1-34 cRES>
A;Cross-references: GB:S77806; NID:999891; PIDN:AAB34076.1; PID:999892
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Conservative 1; Mismatches 6; Indels
                                                                                              retinoic acid receptor homolog - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
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Best Local Similarity
Matches 10; Conserv
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                                       A;Molecule type: DNA'
A;Residues: 1-31 <STO>
A;Residues: 1-31 <STO>
Cross-references: UNIPROT:Q9HWH1; GB:AE004437; NID:g10581935; PIDN:AAG20600.1; GSPDB:G
C;Genetics:
A;Gene: VNG2544H
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C;Genetics:
A;Gene: AGR C:
A;Map position: circular chromosome
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R,Johnson, D.; Gattung, S.
Bubmitted to the EMBL Data Library, November 1995
A,Reference number: 220655
A,Reference number: 220658
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Residues: 1-31 < JOH>
A,Residues: 1-31 < JOH>
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29628
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Pred. No. 1.4e+04;
8; Mismatches 4; Indels
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Best Local Similarity 32.6%;
Matches 14; Conservative 8
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-31 <KUR>
A;Status: preliminary
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Sequence 4, Appli
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(without alignments)
1403.926 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
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US-09-902-540-9932
US-09-902-540-10304
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US-08-474-657-9
US-08-474-667-9
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US-08-474-667-9
US-08-474-667-9
US-08-474-461-8
US-09-479-4677-15
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US-09-9479-4677-10
US-09-9479-4677-10
US-09-9479-467-10
US-09-949-016-10933
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US-08-793-273C-4
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                                                                                                                                                                                              October 12, 2005, 10:00:24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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26 4, Appli 26 2, Appli 26 2, Appli 26 8, Appli 26 8, Appli 26 6, Appli 26 6, Appli 26 6, Appli 26 6, Appli 26 10208, A 26 11378, Ap 26 1378, Appli 27 4, Appli 28 2, Appli 29 2, Appli	melanogaster	, Gaps 0 VDYPPVAN 532 1 1 1 2 2
Sequence Seq	Drosophila	imilarity 50.3%; Score 443; DB 4; Length 183; Conservative 22; Mismatches 69; Indels 0; Gaps INGPFIEEKTSVDSPVALED Mismatches 69; Indels 0; Gaps INGPFIEEKTSVDSPVALED Mismatches 69; Indels 0; Gaps INGPFIEEKTSVDSPVALED MISMATCHIPLINAVDYPPVAN
790-912-4 658-136-5 476-71-2 470-467A-2 652-469-8 422-582-8 052-469-6 912-540-10208 902-540-1084 912-540-11984 918-352-5503 318-352-5503 978-277A-4 449-644-2 668-44A-2	rs ceins of	3; DB 4; tches 69 tches 69 FELTVTDSDG I.YEWSLGPGS I.YEW
- 08 - 790 - 912 - 08 - 68 - 136 - 08 - 68 - 136 - 09 - 470 - 4511 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 09 - 672 - 282 - 08 - 672 -	ALIGNMENTS 70767 and prote 326-094 /270,767	milarity 50.3%; Score 443; DB milarity 50.3%; Pred. No. 1.8e- Conservative 22; Mismatches NGPFIEEKTSVDSPVLRLSNLDPGNYSFRLTVTD
- SU - SU - SU - SU - SU - SU - SU - SU	ALIG tion US/0927076 t al. cleic acids and meference: 7326- MBER: US/09/270 999-03-17 62517 . 2.0	; Sco 22; RLENLD : OLDLTS
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10000000000000000000000000000000000000	8 03K5H N	T.9%; Conservative 22 SPFIEEKTSVDSPVLRLS:
44444444444444444444444444444444444444	767-32456 32456, Applica 5703491 INFORMATION: FINVENTION: NU PERENCE: FILE R APPLICATION: APPLICATION: NI PERENCE: FILE R APPLICATION: SILE R APPLICATION ON SILE SILE R APPLICATION ON SILE SILE SILE R APPLICATION ON SILE SILE SILE SILE SILE SILE SILE SILE	Similarity 50.3%; 92; Conservative 22; 92; Conservative 23; 1 INGPFIEEKTSVDSPVLRLG;
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00000000000000000000000000000000000000	RESULT 1 US-09-270-7 Sequence Patent No. GENERAL TITLE OI FILE REI CURRENT CURRENT CURRENT SOFTWARI SOFTWARI SEQ ID. NO. TYPE: 1 TYPE: 1 TYPE: 0 CORGENT CORRE	Query Matches Matches Matches Oy Db Oy Oy Db Oy Ay Cy Ay Db Db Db Db Db Db Db Db Db Db Db Db Db

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Keith Weinstock et al

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117 VIVWTQI-GGTPVTLSDASSLTPTFTAPASSDPLTFLLMVSD-----GTATVVDVTSISV 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 EYXDDYR----ELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSVGDSPAVPAETQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 KEV--LMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSES-TPSEL- 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832 LIYLWIQVSGTPVAVKDYTTPTATFIAPEVTLDESLVFRLIVSDGIATVNDTVTVTVTNA 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    588 DFEDDYDGATVEISED------GGQTWVDIG-----DPIHNSVLETYPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 ODPELHYLNESASTPA----PKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQSSNSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------PISPT-----LTVSAG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98; Mismatches 291; Indels 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1300;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.6%; Score 312; DB 4; Best Local Similarity 23.9%; Pred. No. 1.5e-15; Matches 184; Conservative 98; Mismatches 291.
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9932
LENGTH: 1300
                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                             US-09-902-540-9932
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17307
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Sequence 17307, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION:

US-09-248-796A-17307

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; Sequence 5, Application US/08061376; Patent No. 6175000
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APPLICANT: Glidman, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 5001-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 13786
LENGTH: 1093
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                                                                                                                                                                                                                                                                                                                      DB 4; Length 372;
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: HIGHLA, GREGOTY J.
APPLICANT: HIGHLA, GREGOTY J.
APPLICANT: MIGGAIA, Reven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and UFILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
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25.1%; Pred. No. 5.3e-08;
iive 58; Mismatches 144;
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                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10204
LENGTH: 372
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                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 86; Conserv
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GENERAL INFORMATION:

APPLICANT: Byans, Glen A.

APPLICANT: Byans, Glen A.

APPLICANT: Selleri, Licia

APPLICANT: Parry, Pauline

TITLE OF INVENTION: CHARCTERIZATION OF A CHROWOSOME 11023

TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
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                                                                                                       494 LDPGNYSPRLTVTDS-------DGATNSTT------AALIVNNAVDYPPVA
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L-PERSVLL------PLPTT------PSSGEVLEKEKASQLQE----
                                                                                                                                                                                                                                                                                       ----QSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAP
                                                                                                                                                                                                                                                                                                                                       352 QAHPFQEAQDRMKHYLVAGYKATPVS---PTFLEARDALLAVTAAS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GVQTPYLHLSAMQEGDYTFQL---KVTDSSRQQSTAXVTVIVQPEN---NRPPVAVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 PD-----KELIFPVESA----TLDGSSSSDDHG-IVFYHWEHVRGPSAVEMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --NAFGEGFVNVTVKPARRVNLPPVAVVSPQL--QELTLPLTSAL-----
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3468 QRDLDSASGPQVSNFTQTVDAPNSMGLEQNKALSSAVQASPTSP-----GG-----SP 3515
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                                                                                                                                                                                                                                                 3427 VLPSTQTTGITAASP-----SGEADEH----YQLQHVNQLLASKTGIHSS 3467
                                              334 ASSSSVLNVVSMQTTTTPTSSÄSVPGHVTLTNPRLLGTPDIGSISNLLIKASQQSLGIQD 3393
                                                                                                                                              3394 QPVAL-----PPSSGMFPQLGTSQTP---------STAAITAASSIC 3426
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3516 SSPSSGQRSA------SPSVPGPTKPKPKTKRFQLPLDKGNGKKHKVS--- 3557
---NSITLNGNQSS---DD 556
                                                                                                                                                                                                  617 VOPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRG--PSAVEMENI 674
                                                                                                                                                                                                                                                                                                675 DKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNN 734
                                                                                                                                                                                                                                                                                                                                                                                                  -- DVIDGSDHSVALQL 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------HLRTSSEAHIPDQETTSLTSGTGTPGAEAEQQDTASVE-QSSQKECG 3604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ASDIDIAIVEVQPDPRKSG 816
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                                                                                                  557 HOIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parent No. 6753314
GENERAL INFORMATION:
PAPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
TITLE OF INVENTION: 15966-542
CURRENT APPLICATION NUMBER: 00/102/29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/179,965
PRIOR FILING DATE: 2000-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q03164
US-09-538-092-1262
  512 TNSTTAALIVNNAVDYPPVANAG-PNH-TITLPQ----
                                                                                                                                                                                                                                                                                                                                                                                                     735 SITLDGSRSTDDQRIVSYLWIRDGQSPAAG----
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SOFTWARE: CuraPatSeqFormatter Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1262, Application US/09538092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NLPPVAVVSPQ-LQELT---LPLTSALID-GSQSTDDTEIVSYHWEEINGP 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 KLPERSVLLP--LPTTPSSGE----VLEKEKASQLQEQSSNSSGKEV----LMPSH--- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SLPP-ASLEL-----SSVTVEKSPVLTVTPGSTEHSIPTPPTSAAP 313
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                                      iSEE: Pretty, Schroeder, Brueggemann & Clark
1: 444 South Flower Street, Suite 2000
Los Angeles
California
                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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3.3%; Score 184.5; DB 3;
Best Local Similarity 20.2%; Pred. No. 0.00016;
Matches 181; Conservative 115; Mismatches 273;
                                                                                                                                                                                                                                                                                                       SOFTWARE: FOLLIAL STATES SOFTWARE: FOLLIAL APPLICATION NUMBER: US/08/061,376 FILING DATE: 13-MAY-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Releter, Steephen E. REGISTRATION NUMBER: 31,192 REFERENCE/DOCKET NUMBER: 941 9387 TELEPHONE: (619)546-4737 TELEPHONE: (619)546-9392; INFORMATION: 7 TELEPAX: (619)546-9392; INFORMATION: 9820 ID NO: 5: SEQUENCE CHARACTERISTICS:
                    CORRESPONDENCE ADDRESS:
ADDRESSES: Pretty, Sch
STREET: 444 South Flow
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: unknown
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US-08-474-067-9
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                                                                            3117 TNTSVLGPMGGGLTLTTGLNPSLPTSQSLFPSASKGLLPMSHHQHLHSFPAATQSSFPPN 3176
                                                                                                                                 1284 NIIKRSKSSIMYFEPAPLLPQSVGGTAATAAGTSTISQDTSHLTSGSVS-----GL 3334
                                                                                                                                                                                                                                                                                                                          3335 ASSSSVINVVSMQTTTTPTSSASVPGHVTLTNPRLLGTPDIGSISNLLIKASQQSLGIQD 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSPSSGORSA----SPSVPGPTKPKPKTKRFQLPLDKGNGKKHKVS--- 3558
                                                                                                                                                                                                                                                                                                                                                                                                   3395 QPVAL-----PPSSGMFPQLGTSQTP-------STAAITAASSIC 3427
                                                                                                                                                                                                                                         512 TNSTTAALIVNNAVDYPPVANAG-PNH-TITLPQ------NSITLNGNQSS---DD 556
                                                                                                                                                                                                                                                                                                                                                                     557 HQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXVTVI 616
                                                                                                                                                                                                                                                                                                                                                                                                                                  617 VQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRG--PSAVEMENI 674
                                              TY-----NYEWNLISHPIDYQGEIKQGHKQTL-----N 394
                                                                                                                                                                          -----NLPPVAVVSPQ-LQELT---LPLTSALID-GSQSTDDTEIVSYHWEEINGP 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                675 DKAIATVTGLQYGTYHFRLTVKDQQGLSSTSTLTVAYKKENNSPPRARAGGRHVLVLPNN 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITLDGSRSTDDQRIVSYLWIRDGQSPAAG-------DVIDGSDHSVALQL 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             779 INLVEGVYTFHLRVTDSQG------ASDIDTATVEVQPDPRKSG 816
                                                                                                           LSQLSVGLYV------KKVTVSSENAFGEGFVNVTV------KPARRV----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,067
FILING DATE: 07-UNN-1995
TARGIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
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Patent No. 5811518
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 ADSPP-EGVFTIEKESGWILLIHMPLDREKIVKYELYGHAVSENGASVEEPMNI-SIIVTD 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 839 RQLAV--LLNVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 SY--HWBEINGPF----IBEKTSVDSPVLRLSNLDPGNY-SFRLTV--TDSDGATNSTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.3%; Score 183.5; DB 2; Best Local Similarity 21.4%; Pred. No. 1.4e-05; Matches 165; Conservative 90; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31, 815
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9099
INFORMATION FOR EGG ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
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951 NCEWSIFYVTVLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELR 1010
-----TATATVVVHVKDVNEAP------VFVPPSKVIEAQEGIS 446
                                                                                                                                               779 TNLVEGVYTFHLRVTDSQCASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLV 838
                                                                                                                                                                                              501 --VKANNYEVMVLATDSGNPPTTGTGTL-----LLTLTLTDINDHGPIPEPRQIIIC 548
                                                                                                                                                                                                                                                  839 RQLAV--LLINVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVLKAAEVARNLHMRLSKE 896
                                                                                                                                                                                                                                                                               897 KADFL---LFKVLRVDTAGCLLKCSGHGHCDPLT--KRCICS-HLWMENLIQRYIWDGES 950
                                                                           | : : | : | | : | | : | | 648 -----KVKEPLLPEDD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,481

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/213,361

FILING DATE: 14-MAY-1994

PRIOR APPLICATION NUMBER: US 08/213,361

FILING DATE: 30-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REFERENCE/POCKET NUMBER: 9-LJ 1686

TELECOMMUNICATION NUMBER: 9-LJ 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08472481
Patent No. 5863804
GENERAL INFORMATION:
APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
UNDMER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.3%;
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CITY: San Diego
STATE: California
COUNTRY: United States
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 822;
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/474,068A
FILING DATE: 07-UNN-1995
CLASSIFICATION: 514
                                                                 GENERAL INFORMATION:
APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                            3: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260;
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3.3%; Score 183.5; DB 2
Best Local Similarity 21.4%; Pred. No. 1.4e-05;
Matches 165; Conservative 90; Mismatches 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-007-1990
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31, 915
REFERENCE/DOCKET NUMBER: P-LJ 1683
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 535-9001
TELEPRONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9;
                  Sequence 9, Application US/08474068A
Patent No. 5837525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 822 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                             CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
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APPLICANT:
APPLICANT:
BAT, MAUREEN M.
TITLE OF INVENTION:
POLYCYSTIC KIDNEY DISEASE GENE HOWOLOGS REQUIRED FOR MALE MAT
TITLE OF INVENTION:
BEHAVIOR IN NEMATODES AND ASSAYS BASED THEREON
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/09/479,467A
CURRENT FILING DATE: 2000-01-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ::| | ::| | ::| | 673 TSSTPSTLS-TSTUBSSTRSSDSTTTSAGSTTTLQESTTTSESSTTDSSTTTIS
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                                                                                                                                                                             PTSTASTSTSTSTTOO-----SSSTITSSPSSTTLSTSIPTTTTPEITSTLSSLPDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                    LKAFVA--PAPPVETTYNYEWNLISHPT------DYQGEIKQGHKQTLNLSQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKATTTFYDSTSVNLTLNSGLG11GYQTSIECTSPTSSNYVSTTKDGACFTKSVSMPRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----POLOELTLPLISALIDGS--OSTODTEIVSYHWEEI-NGPFIEEKTSVDSPVLRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVA-NAGPNHTITLPQNSITLN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GNOSSDDHQIVL----YEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLKVTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             658 YHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAV--KKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: | | | | | | | :: | AICSYLDETTTETTTTMLTSTTTTEPSTSSTVTTTEPTTTLTTSTAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LSVGLYVFKVTVSSE-----NAFGEGFVNVTVKPARRVNLPPVAVVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOTFECRNVSTEPFLIIKESTCLNYSNTVLNATYSSNIPIQPIETFLVGI-----GTYEF
                                                                                                                                                                                                                                                                                         ASLELSSVIVEKSP----VLTVTPGSTEHSIPTPPTSAAPSESTPSELPISPTTAP---
                                                                                                                                           FNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVL-
                                                                     Length 2870;
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TXDSSUTITDSSNST-----
                                                                   Query Match 3.3%; Score 183.5; DB 4;
Best Local Similarity 19.4%; Pred. No. 0.00011;
Matches 147; Conservative 97; Mismatches 259;
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                  Elegans Lov-1 sy582 deletion protein
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     ; TYPE: PRT
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US-09-479-467A-15
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APPLICANT: Sternberg, Paul W.
APPLICANT: Barr, Maureen M.
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENB HOMOLOGS REQUIRED FOR MALE M.
TITLE OF INVENTION: BEHAVIOR IN NEMATODES AND ASSAYS BASED THEREON
TITLE OF INVENTION: BEHAVIOR IN NEMATODES AND ASSAYS BASED THEREON
TITLE OF INVENTION: 18021-2901B
CURRENT FILING DATE: 1809-01-06
CURRENT FILING DATE: 060/115,127
PRIOR FILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 16
SSOTHARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 2870
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US-09-479-467A-15
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   60/115,127
                           PRIOR FILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 3178
TYPE: PRT
ORGANIOM: C. Rlegans Lov-1 protein
PRIOR APPLICATION NUMBER:
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RESULT 13
US-09-949-016-9270
Sequence 9270, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELLING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 9270
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                                                                                                                                                                                                                                                                                                                                                               3.3%; Score 183; DB 4; Length 2254;
20.8%; Pred. No. 8.2e-05;
ive 83; Mismatches 302; Indels 276;
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                                                                                                                                                                                                                                                                                                                                                                                                    Matches 174; Conservative
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US-09-949-016-9270
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Best Local
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Sequence 30227, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
THE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: US 60/074,788
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30227
LENGTH: 2736
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758 VPTVVGDRPDTNVPGDHVATVEVTYPDĞTKDİVEVİTVHVTPKPVPDKDKYDÈ----TĠĠ-
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      678 IATVTGLQ-----VGTYHFRLTVKDQQGLSSTSTLTVAV-----KKENNSPPRARAGGR
                                                                                                                                 HVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVY
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                                                                                                                                                                                                                                                              787 TFHLRVTDSQGASDTDTATVEVQPDP 812
                                                                                                                                                                                                                                                                                                                           857 VATVEVŤYPDĠTXĎŤVEVŤVHÝTPKP 882
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US-09-252-991A-30227
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APPLICANT: LINDAHL, Gunnar
APPLICANT: STALHAWMAR-CARLEMALM, Margaretha
APPLICANT: STALHAWMAR-CARLEMALM, Margaretha
APPLICANT: STALHAWMAR-CARLEMALM, Margaretha
TITLE OF INVENTION: PROTEIN RIB, A CELL SURFACE PROTEIN THAT CONFERS IMMUNITY TO MANY
TITLE OF INVENTION: OF THE GROUP B STREPTOCOCCUS: PROCESS FOR PURIFICATION OF THE PR
TITLE OF INVENTION: AIT AND PHARMACEUTICAL COMPOSITION
FILE REFERENCE: 052-0140P
CURRENT APPLICATION NUMBER: US/09/434,123A
CURRENT PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
1906 GLDPAHRYKLLLYGLHHGKRVGPISAVAITAGREETETETTAPTPPAPEPHLGELTVEEA 1965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.3%; Score 182.5; DB 4; Length 1020;
22.4%; Pred. No. 2.4e-05;
tive 83; Mismatches 307; Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Group B Streptococcus - Strain A909
US-09-434-123A-9
                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09434123A
Patent No. 6586580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 22.4
Matches 167; Conservative
                                                                                                                                                                                                                                                              -09-434-123A-9
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1494	649	1553	108	1587	191	1631	820	1690		
1463 GQVTADGSGNWSFTPGIPLPDGTVVNVARSP 1494	SSRQQSTAXVIVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSS		650 SDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQG-LSSTSTLT 708	THE TELEPTE TO THE TELEPTE THE TELEPTE TO THE TELEP	709 VAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDV-I 767	1588 VDAIAPPAPVINPSNGVVISGTAEAGATVILTDGNGNPIGQVTA 1631	768 DGSDHSVALQLINLVEGVYTFHLRVTDSQGASDTDT-ATVE-VQPDPRKSGLVEL 820	DESCRWAPTPATPLANGT-VINALAQDAAGNNSSPTSATVDSLAPAAPVIDPSNGSVIAG 1690	821 TLQVGVGQLT 830	i i i i i i i i i i
1463	604	1495	650	1554	709	1588	168	1632	821	1691
QQ	ò	qa	δλ	q	ò	qq	ò	qq	ò	q

Search completed: October 12, 2005, 10:19:17 Job time : 62 secs

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GenCore version 5.1.6
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                  Copyright
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- protein search, using sw model OM protein October 12, 2005, 10:00:24 Run on:

; Search time 52 Seconds (without alignments) 1983.546 Million cell updates/sec

US-10-764-390-3 5580 Title: Perfect score:

1 MAPPIGVLSSLLLLVTIAGC......VSMNGSIRNGASFSYCSKDR 1072 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

seq length: 0 seq length: 200000000 88 Minimum Maximum

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* 79:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	Length	DB	dī	Description
1	225	4.0	26926	<u> </u>	I38344	titin, cardiac mus
7	208.5			~	820901	•
٣	208	3.7		7	F90696	hetical pr
4	205	•		~	S24600	44
Ŋ	203.5	3.6		7	B85547	probable RTX famil
9	202.5	3.6		7	T13931	projectin - fruit
7	201.5	3.6		~	AC1018	eti
Φ	200.5	3.6		~	D82510	
Ø.	200.5	3.6		~	C64483	hypothetical prote
10	195.5	3.5		~	A46405	ш
11	195.5	3.5		~	T34434	hypothetical prote
12	192.5	3.4		7	146521	titin - rabbit (fr
13	190.5	3.4	٦	~	E90696	hypothetical prote
14	190.5	3.4		~	A85547	
15	190	3.4	m	7	AH2493	
16	188	3.4		~	147141	gastric mucin (clo
17	188	3.4		~	T09070	probable tenascin
18	187.5	3.4		~	T34513	hypothetical prote
19	187	3.4		~	AI1489	probable peptidogl
20	187	3.4	3624	~	AD0835	large repetitive p
21	186	3.3	~	7	A54849	collagen alpha 1(V
22	184.5	3.3		Н	IJMSCP	P-cacherin precurs
23	183	3.3	φ	~	A88852	protein unc-22 [im
24	183	3.3	φ	~	S57242	twitchin [similari
25	183	3.3	7	~	T27935	hypothetical prote
56	182.5	3.3	-	~	T33369	hypothetical prote
27	181.5	3.3	3968	~	A44265	
28	179	3.2	S	N	T20992	hypothetical prote
29	179	3.5	5198	0	T43290	hemicentin precurs

heparan sulfate pr probable translati glucan 1,4 alpha-g zonadhesin - mouse tenascin-X - bovin ankyrin 3, long sp hypothetical prote probable oligopept peptidoglycan link zinc finger protei probable peptidogl tenascin-X precurs	proline-rich pepti projectin - fruit hypothetical prote fibronectin - bovi
\$18252 109072 148478 144215 1426215 1426215 1426215 67272 672730 672730 672730 672730 672730 672730 672730	A41819 A40985 T25697 FNBO
001000000000	1000
3707 1666 1367 5376 4135 4377 2468 802 1711 1701 2013	5762 940 1229 2265
178.5 177.5 177.5 176.5 176.5 176.5 178.1 173.5 173.5	173 172.5 172.5 172
	4 4 4 4 0 W 4 N

ALIGNMENTS

```
C;Species: Homo sapiens (man)
C;Species: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text change 09-Jul-2004
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text change 09-Jul-2004
C;Accession: 138344; 138345; $20898; $20897; $20899; $63565; $37393
R;Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330; PMID:7569978
                                    N;Alternate names: connectin
N;Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)
cardiac muscle [validated] - human
```

A; Accession: 138344

A,Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMB A,Molecule type: mRNA A,Residues; 1-26926 (LAB1).
A,Residues; 1-26926 (LAB1).
A,Cross-references: UNIPROT:010466; EMBL:X90568; NID:g1017424; PID:g1017425
B,Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.
Biochemistry 34, 553-561, 1995
B,Title: Dissecting titin into its structural motifs: identification of an alpha-helix m A,Reference number: 138345; MUID:95119041; PMID:7819249

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: 1977-2014 (MUS>
A;Cross-references: BMBL:X83270; NID:g602579; PIDN:CAA58243.1; PID:g602580
A;Note: conformation and properties are reported for a synthetic peptide corresponding t R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
BMBO J. 11, 1711-1716, 1992
A;Title: Towards a molecular understanding of titin.
A;Reference number: S20897; MUID:92258380; PMID:1582406

A;Accession: S20898
A;Status: nucleic acid sequence not shown
A;Nolecule type: mRNA
A;Residues: 13597-14200, 17,14202-14696 <1AB2>
A;Cross-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193
A;Accession: S20897
A;Status: nucleic acid sequence not shown; translation not shown

A;Residues: 16330-16382,'S',16384-16756,'F',16758-16860 <LAB3> A;Cross-references: BMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191 A;Accession: S20899 A; Molecule type: mRNA

A,Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: mRNA A; Residues: 'P', 22378-22431,'R', 22433-22448,'G', 22450-22453,'Q', 22455-22480,'TR', 22483-2 A; Residues: 'P', 22278-223431,'R', 22433-22448,'G', 22450-22453,'Q', 22455-22480,'TR', 22483-2 A; Cross-references: EMBL:X64697; NID:931190; PIDN:CAA4538.1; PID:937195 B; Kolmerer, B:, Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S. J. Mol. Biol. 256, 556-563, 1996 J. Mol. Biol. 256, 556-563, 1996 A; Title: Genomic organization of M line titin and its tissue-specific expression in two A; Reference number: \$63665; MUID:96177761; PMID:8604138

A; Status: nucleic acid sequence not shown

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14084 SNVT--KNTATVSWKRPVDDGGSEITGYHVERREKKSLRWVRAIKTPVSDLRCKVTGLQE 14141
                                                                                                                                                                                                                                                                                                                                                                                                                      14201 YDGGLEITGYVVEHQKVGDEAWIKDTTGTALRITQFVVPDLQTKEKYNPRISAINDAGVG 14260
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A; Wolecule type: DNA
A, Readude: 5729-2625 < KOLD.
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A, Readude: 2729-2625 < KOLD.
A, Cross-references: EMBL:X92412; NID:g1236761
R; Gautel, M.; Leonard, K.; Labeat, S.
EMBO. 7. 12, 3817-384, 1993
A, Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differentiat A, Recession: 831793; MUD:94008990; PMID:8404852
A, Phosphorylation of KSP motifs in the C-terminal region of titin in differentiat A, Recession: 831793; MUD:94008990; PMID:8404852
A, Rocession: 831793; MUD:94008990; PMID:8404852
A, Rocession: 831793
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R; Improca, S.; Politou, A.S.; Pastore, A.
R; Monitted to the Brookhaven Protein Data Bank, Repruary 1996
A, Reference number: A66736; PDB:1ITT
A, Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
A, Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155
C, Genetics:
A, Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155
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A, Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155
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F;26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 -----SGEVLEKE-----KAS-----KAS-----QLQEQSSNSSGKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 SESTPS---ELPISPITAPRIVK------ELIVSAG-----DNLIITL-----PDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QELTLPLTSALIDGSQSTDD--TEIVSYHWEEINGPFIEEKTSVDSPV----LRLSNLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 IRKOLXFLGKOWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SSVGDSPAVPAE--TQQDPELHYLNESASTPAPKLPE-----RSVLLPLPTTPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 IKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNL--PPVAVVSPQL
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4.0%; Score 225; DB 1; Length 26926;
Best Local Similarity 19.5%; Pred. No. 0.027;
Matches 254; Conservative 186; Mismatches 414; Indels 448; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  =
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----T 14714

titin - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: 320901; I46520
R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
BMBO J. 11, 1711-1716, 1992
A;Title: Towards a molecular understanding of titin.
A;Reference number: S20897; MUD:92288380; PMID:1582406
A;Accession: S20901
A;Reference number: S20897; MUD:92288380; PMID:1582406
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A SEALER CARRIED DATION OF two types of 100-residue motif in the sequence of titti A. Reference number: 146220, MUID-90238553; PMID-2129545 A. A. Resented annumber: 146220, MUID-90238553; PMID-2129546 A. Resented annumber: 146220, MUID-90238553; PMID-2129546 A. Resented annumber: 146220, MUID-90238553; PMID-2129546 A. Resented annumber: 146220, MUID-90238553; PMID-2129546 A. Resented annumber: 146220, MUID-9023853; PMID-2129546 A. Resented annumber: 146220, MUID-9023853; PMID-90297; Length Re605; Length Ref065; Le	1429 654 1481 703 1536 719 1596	SSD 556	DPGNYSF 501 Qy 250 KEKASQLQEQSSN	-SPOLOB 444 QY 190 GSEGAFNSSVODS ::	QLGSVGLY 403 Query Match :: : : : ILCTLELF 1218 Matches 173; Conservati	346	286 1124	- 249 T 1064		138 VTK 964	OY 865 TVIVEYVQSRPPF	Gaps 59;	pro Db 1711	Db 1657 VKEISRDSAYITW	
ក្រុមក្រុមក្រុមក្រុម ខ្លុំ ប្		0 0 1	S LTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFI : : : : : GGSEITNYIVDKRETSSRNWAQV	4 0	7 8	2 7	0 10	3 GAFNSSVGDSPAVPAETQQ : 4 YSF	மை	KKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNR 	52 FPVVDCTAACCDLS	3.7%; Score 208.5; DB 2; Length 6 imilarity 18.8%; Pred. No. 0.029; ; Conservative 155; Mismatches 363; Indels	iss-references: EMBL:X17329; NID:g1756; PIDN:CAA35207.1; PID:g ^s :erfamily: titin; fibronectin type III repeat homology; immunoc words: muscle	tus: translated from GB/EMBL/DDBJ ecule type: mRNA idines: 4735_5546 7135>	le: A regular pattern of two types of 100-residue motif in the erence number: 146520; MUID:9023853; PMID:2129545 ession: 146520

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42 [imported] - Escherichia coli (strain O157:H7, substrain RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equence of enterohemorrhagic Escherichia coli 0157:H7 and geno; WUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71:Q8X2T1; GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:Grain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.7%; Score 208; DB 2; Length 5291;
20.6%; Pred. No. 0.021;
ive 114; Mismatches 319; Indels 234; Gaps 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISDDAINAAEKGAALTLSGSTSGVEAGQTVTVTFGGKTYTTTVAANG 3188
                              :|: : :|| :: || SSTASHNVQVNTALPGITIN----PVATDDIINASEAGSAQTISGQVT 2963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGVIVSGISTAQIGQILIVILNGI----NYQITVQIDGSWSL---- 3291
                                                                                        RVTDSQG------PDPR 813
                                                                                                                                                                          VGQLTEQRK-DTLVRQLAVLLNVLDSD-----IKVQKIRAHSDLS 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPAVPAETQODPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVLE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PISPTTAPRTVKELTVSAGDNLIITLP-----DNEVELKAFVA-- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVSPQLQELT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TRIVSYHWE-----BING 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLRLSNIDPGNYSFRLTVTDSDGATNSTTAA------LIVNNAV 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GPNHTITLPQNSITLNGNQSSDDHQIVLY---EWSLGPGSEG 572
DDQRIVSYLWIRDGQSPAAGDVIDGSD------HSVALQLT 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nce_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                             --VAKDDVVAPDLDLKDLPDLCYLAKENSNFRL 1864
                                                                                                                                                                                                                                                                        PKVLKAAEVARNLHMR-----LISKEKADFLL 902
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us-10-764-390-3.rpr

STA IETPDXYTKLVIRPTQRSDSGEYLVTATNTSGKDSVLVNVVITDKPSPPNG		Operation Control Co	XFI XFI	
573 KHVVMQGVQTPYLHL 3292TLPASDL 630 GPDKELIFPV 3342 GDDVINNVEHTQAQI 685 QVGTYHFRLTVKDQQ 685 QVGTYHFRLTVKDQQ 3402 ADGTVTISATITDSA 734 NSITLDGSRSTDDQR	3453 SALILESGI	RESULT 4 S24600 projectin - fruit fly (Drosop Cispecies: Drosophila melanog Cispecies: Drosophila melanog Cispecies: Drosophila melanog Cispecies: Drosophila melanog Cispecies: Dreb-1995 #sequence Cispecies: S24600 A, Accession: S24600 A, Accession: S24600 A, Status: preliminary A, Wolecule type: mRNA A, Residues: 1-1742 < FYRS A, Cross-references: UNIPROT: Q Cispenetics: A, Genetics: A, Genetics: A, Genetics: S1yBase: F A, Cross-references: FlyBase: F	187, CONSERVATIVE 187, CONSERVATIVE 133 VSEVHKDGCKLKWKK 133 SPEDIRKDLXFLGKOD 172 193 GAFNSSVGDSP 193 YKFRVKAVNKEGESE	235 LIPLPTTPSSG 243 AWPEPASDGGSPIQG 290 SPVLTV 281 -PTATVGGLIEGNEY 333 KELTVSAGDNLIITL : : : :

QY 99 YLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRKDL 141 DD 2468 YTKLVIRPPQRTDSGEYLVTATNTSGKDSVLVNVYITDKPSPPNGPLQISDVHKEG 2523 OY 142 XFLGKDWGLEEMSEXXDDYRELEKDLLQP-SGKQEPRGSAEYTD-WGLLPGSE 192	2524 CHL 193 GAF	A 6	2626 AWTPPVIDGGSPISCYIIĒKQDKYGKWĒRALDVPADQCKATIPDĪVEGĢTYKF 267 291 PVLTVTPGSTEHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNL 343		2726 TFDCKVSGEPÄPQTKWLLKKKEVÝSKD-NVKVTNVDÝNTKLKVNSATR 398 LSVGLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVSPQLQELTLPLT :			TAQAIIAKNPPDVPTKP-GTPT VWQGVQTPYLHLSA	KRDKFSPDWEKCAEISDDITIAH'PDLIEGLKYEF NNRPPVAVAGPDKELIFPVESATLDG		Db 3038WTHEGNMIINTDRVKISNPEDBRTKIRILSATS-DTGYYTLTARINGTDRHNVK 3090 Oy 708 TVAVKKENNSPRARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWI 755 Db 3091 VTILDAPSVPEPALRNGDVSKNSIVLRWRPPKDDGGSEITHTVVEKMDNEAWRWW 3145 OY 756 RDGQSPAAGDVIDGSDHSVALQLTNLVEG-VYTFHLRVTDSQGASDTDTATVEV 808 1146PVGDCTDTEIRADNLIENHDYSFRVRAVNKQGQSQPLTTSQPITAKDPY 3194 OY 809 -QPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVI 867
Db 2964 GAAAGSTVTVELGGKTYTATVQADLSWNVSVPAADWQALGNGELTVNASVTNA 3016 Oy 360PAPPVETTYNYE-WNLISHPTDYQGEIKQG 388 Db 3017 VGNTGSGTRDITIDASLPGLAVDTVAGDVVNIIEAAOAOLIYGSSGSPAAGTALTV 3073	389HKQTLNLSQLSVGLYVFKVTVSSENAFGEGFVNVTVFPARRVNLPPVAVVSPQLQELT 446 1	Qy 447 LPLTSALIDGSQSTDDTION TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TOTAL TO THE TOTAL THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TO THE TOTAL TOT	QY 476 PPIEEKTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAV 525 DI :	Qy 526 DYPPVANAGPNHTITLPQNSITLNGNQSSDDHQIVLYEWSLGFGSEG 572 D) S 242 ASDNIINASEAAAGVTVSGTSTAQTGQTLTVTLNGTNYQTTVQTDGSWSL 3291 Q	QY 573 KHVVMQCVQTPYLHLSAMQEGDYTFQLKVTDSSRQOSTAXVTVIVQPENNRPPVAVA 629 D) DD 3292TLPASDLTALANNGYTLTATVSDLAGNLGSASKGVTVDTTAPVISFNTVA 3341 Q	630 GPDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGFSAVEMENIDKAIATVTGL 684	OY 685 CVGITHERLIVALQQGLSSISILIVAVRAENDSFFRARAGGRAVLALEN /33	QY 734 NSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQ	Qy 778 -LINLVEGV-YTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQV-GVGQL-TEQR 833 D) 3497 DVAALSDGTSYTVSASAQDSAGNSATASRSVAVDLTAPVISINTVSTDDR 3546 Q	Cy 834 KDTLVRQLAVLIAN 846 Db 3547 XNAAEQQQPLTLAN 3559	RESULT 6 T1391 projectin - fruit fly (Drosophila melanogaster) (fragment) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Accession: T13931 R;Daley, J; Southgate, R:, Ayme-Southgate, A. Nol. 219. 201-210, 1998 A;Title: Structure of the Drosophila projectin protein: isoforms and implication for profesterence number: Z17815; MUD199300339; PMID:9636710 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Gones: Lefs a cDAL> A;Gones: Lefs a cDAL> A;Gones: Teferences: FlyBase: FBgn0005666 A;Accession: T13931 A;Accession: T1393 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Accession: T13931 A;Ac

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C6483

C9483

C9483

Cypotherical protein MJ1468 - Methanococcus jannaschii

C,Species: Methanococcus jannaschii

C,Species: Methanococcus jannaschii

C,Decies: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Ju1-2004

C,Accession: C6483

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

R;Bult, C.J.; White, O.; Olsen, G.J.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;

Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Ouail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A; Reference number: ABO502; MUID:21534947; PMID:11677608
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-3283 < PAR>A; Residues: 1-3283 < PAR>A; Cross-references: GB:AL513382; PIDN:CAD09244.1; PID:g16505248; GSPDB:GN00176
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Live 99; Mismatches 245;
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Best Local Similarity 20.5%;
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23.8%; Pred. No. 0.0038;
tive 67; Mismatches 187; Indels 105;
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A;Map position: 2
C;Superfamily: chitinase with C-terminal chitin-binding domain
3192 ADGSYTFTVTVTDVAG 3207
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Best Local Similarity 23.8%
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A46405
C protein alpha antigen - Streptococcus sp. (strain A909, group B, type Ic)
C;Species: Streptococcus sp.
C;Date: 21.Sep-1993 #sequence revision 20.Sep-1999 #text_change 03-Nov-2000
C;Accession: A46405, B46405; T30854
E;Michel, J.L.; Madoff, L.C.; Olson, K.; Kling, D.E.; Kasper, D.L.; Ausubel, F.M.
Proc. Natl. Acad. Sci. U.S.A. 89, 10060-10064, 1992
A;Title: Large, identical, tandem repeating units in the C protein alpha antigen gene, b A;Reference number: A46405; MulD:93066179; PMID:1438195
A;Accession: A46405
A;Residues: 1-1020
A;Residues: 1-1020
A;Cross-references: GB:M97256; NID:9153558; PIDN:AAA26848:1; PID:9153559
A;Note: sequence extracted from NCBI backbone (NCBIN:117590, NCBIN:117592, NCBIP:117593)
A;Note: the source is designated as Streptococcus agalactiae, group B, strain A909; ATCC
C;Genetics:
     O -A
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: C64483
A;Accession: C64483
A;Actesion: Draiminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-1009 eBUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 TYPDGTKDTVEVTVHVTPKP-VPDKDYGGETTVPQGTPVSDKEITDLVKIPDGSKG
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                                                                                                                                                                                                                                                                                                                                                                                                                       3.5%; Score 195.5; DB 2; Length 23.0%; Pred. No. 0.0093; ative 85; Mismatches 293; Indels
A;Gene: bca
C;Keywords: tandem repeat
F;227-308/Region: 82-residue tandem repeat
F;309-390/Region: 82-residue tandem repeat
F;301-472/Region: 82-residue tandem repeat
F;318-472/Region: 82-residue tandem repeat
F;555-63/Region: 82-residue tandem repeat
F;637-718/Region: 82-residue tandem repeat
F;631-818/Region: 82-residue tandem repeat
F;719-800/Region: 82-residue tandem repeat
F;801-882/Region: 82-residue tandem repeat
F;819-963/Region: 11-residue partial tandem repeat
F;997-1014/Domain: transmembrane #status predicted <TRM>
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       C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Sceisel, C.; Gattung, S.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid K06A9.
A;Reference number: 221525
A;Reference number: 221525
A;Reference number: 221525
A;Rocession: T3444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-223 <GEI>A;Residues: 1-223 <GEI>A;Residues: 1-223 <GEI>A;Residues: 1-223 <GEI>A;Coss-references: UNIPROT:Q8IFX6; EMBL:U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:KCAA;EMBLENCES: C;Genetics: 1-232 <GEI
A;EMBLENCES: C;Genetics: 1-233 <GEI
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 2075/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1069 SASSGSTATMG-----STEASSTSGGSSTS-----PNPSQSTSPSTSGATSSPGSS- 1114
                                                                                                                                                                                                                                                                                                                                                                                                             237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 LPTTPSS------GEVLEKE---KASQLQEQSSNSSGKEVLMPS-HSLPPASLE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     642 EGSTASSPTGSTGSTFSVATEVTSQSTVPSGSSLGTQSTNSS-----PSPSSLSPSTSG 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGD 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 DDTEIVSYHWEEINGPFIEEKTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALI 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  577 MQG-VQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAXV-----TVIVQPENNRPPVAV 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          927 SQSTQTP-----GSTGSTVTQPSTVSDSTSSGSTVTVGSTEGSSSPIPSTSQNTNPSTS 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      629 AG------PDKELIFPVESATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIAT 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              746 GTIMISPSQSSSVGSSQGSTSPAASITS-----GEMTSQGSTQTPG-SSVST 791
                                                                                                                                                                                                                                                                                                                                                                                                             189 PGSEGAFNSSVGDSPA-----VPAETQQDPELHYLNESASTPAPKLPERSVLLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              879 VESSTIPSP---GSPGTILISISPSPSQSTIIGSIQGSI-----SPGISTISEEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                              584 PGSSSTVPSSSSPQPSSQSPAPNTGSTTPSQTSSQSPSPSMNPSSSTPTGS--SQSTITP
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                                                                                                                                                                                                                                                                                                                                      DB 2; Length 2232;
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                                                                                                                                                                                                                                                                                                                                     Query Match 3.5%; Score 195.5; DB 2; Best Local Similarity 21.7%; Pred. No. 0.029; Matches 152; Conservative 75; Mismatches 287;
hypothetical protein K06A9.1a - Caenorhabditis elegans
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RESULT 12

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Cipecies: Orycologue cuniculus (domestic rabbit)
Cipacies: Orycologue cuniculus (domestic rabbit)
Cipacies: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
Cipacession: 146521
Kilabeit, S.; Bazlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.; Francke, U.;
Nature 345, 273-276, 1990
A;Title: A regular pattern of two types of 100-residue motif in the sequence of titin.
A;Reference number: 146520; MUID:90238553; PMID:2129545
A;Accession: 146520; MUID:90238553; PMID:2129545
A;Accession: 146521
A;Accession: 146521
A;Accession: MUID:90238553; PMID:313965
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1000 < LAB>
A;Cross-references: UNIPROT:Q28737; EMBL:X17330; NID:91758; PIDN:CAA35208.1; PID:9930255
C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VMAINLAGVG-KPSLPSEPVVALDP------IDPPGKPEVINVTRNSVTLIWTEPK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LMPSHSLPP--ASLELSSVTVEKSPV----LTVTPGST------EHSIPTPPTSAAP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 SAPSESTGTIICKDEYEAPTIVLDPTIKDGLTIKAGDTIVLNAISILGKPLPKSSWSKAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SESTPS---ELPISPITAPRIVK------BLIVSA-----GDNLIITL-----PDN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVEL-----KAFVAPAPPVE------E 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QELTLPLTSALIDGSQSTDD--TEIVSYHWEEINGPFIE----EKTSVDSPVLRLSNLDP 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GN-YSFRLTVTDSDG-ATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSS 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNTYEFRVSAENRAGIGPPSDASNYVLMKDVAYAPGPPSNARVTDTTKKSASLAWGKPHY 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | | : | | : | | DGGLEITGYVVEHQKYGDETWYKDTIGPALRITEFVVPDLHTKEKYNFRISAINDAGVGE 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QLKVT 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAVIPDVEIVEREMAPDFELDAELRRTLVVRAGLSIRIFVPIKGRPAPEVTWTKDDINLK 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- PPVAVAGPDKELIFPVESATLDGSSSS 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VTGLQVG-TYH 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRVSAENKYGVGEGLKSEPIVAKHPFDVPDAPPPPNIVD-----VRHDSVSLIWTDP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SSVGDSPAVPAE--TQQDPELHYLNESASTPAPKLPE-----RSVLLPLPTTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 YLVSCPHKENC-EPKKMGPIRSYLIFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 IRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDHGIVFYHWE--HVRGPSAVEMENIDKAIAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 3.4%; Score 192.5; DB 2; Similarity 19.8%; Pred. No. 0.013; 91; Conservative 134; Mismatches 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSSRQQSTAXVTVIVQPENNR---
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Db 810 ITKDSVTLHWDLPLIDGGSRITNYIVEKREATRKSYSTVTTKCHKCTYKVTGLSEGCEYP 869 Qy 691 FRLTVKDQQCLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIV 750	
SYLMIRDGQSPAAGDVIDGSDHSVALQLTNLVEG-VYTFHLRVTD	751 SYLWIRDGQSPAAGDHIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGASDTDTATVEVQ 8
Qy 795 SQGAS 799 Db 973 SAGRS 977	RESULT 14 A85547
rain RI	hypothetical protein 20609 [imported] - Escherichia coli (strain 0157:H7, substrain EDL9 C;)Species: Becherichia coli (C;)Species: Becherichia coli (C;)Becie: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;)Accession: A85547 (C;)Accession: A
п, с.б.	Nature 409, 529-533, 2001 A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A.Reference number: A85480; MUID:21074935; PMID:11206551 A.Accession: A85547
DNA Res. 8, 11-22, 2001 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc A; Accession: B90696 A; Accession: E90696 A; Accession: E90696 A; Actus: preliminary A; Molecule type: DNA	A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1461 <sto> A;Cross-references: UNIPROT:Q8XD19; GB:AE005174; NID:g12513364; PIDN:AAG54837.1; GSPDB:G A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics:</sto>
GSPDB:G	Query Match 3.4%; Score 190.5; DB 2; Length 1461; Best Local Similarity 21.1%; Pred. No. 0.029; Matches 139; Conservative 81; Mismatches 214; Indels 225; Gaps 28;
Query Match 3.4%; Score 190.5; DB 2; Length 1461; Best Local Similarity 21.1%; Pred. No. 0.029; Matches 139; Conservative 81; Mismatches 214; Indels 225; Gaps 28;	Qy 191 SEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTTPSSGEVL 248
Qy 191 SEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPTPSSGEVL 248 :	QY 249 EKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEH 302 1
QY 249 EKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEH 302 1	Qy 303 SIPTPPTSAAPSESTPSELDISPTTAPRTVKELTVSAGDNLITLPDNEVELKAFV 358
Qy 303 SIPTPPTSAAPSESTPSELPISPTTAPRIVKELTVSAGDNLIITLPDNEVELKAFV 358	Qy 359 APAPPVETTXNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEG 418
QY 359 APAPPVETTYNYEWNLISHPTDYQGEIKQGHKQTLANLSQLSVGLYVFKVTVSSENAFGEG 418	Qy 419 FUNUTUKPARRUNLPPVAVUSPQLQELTLPLISALIDGSQSTDDTEIVSYHWEEINGPF1 478 ::
QY 419 FVNVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPF1 478 ::	QY 479 EEKTSVDSPVLRLSNLDPGNYSPRLTVTDSDGATNSTTAALIVNNAVDYPPVANA 533
OY 479 EEKTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANA 533	QY 534 GPNHTITLPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEG 593 104 QPGQTVTVTLNGQTXQGVVQPDGTWSVTVPAANVGALADG 743
QY 534 GPNHTITLPQNSITLNGNQSSDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEG 593 Db 704 QPGQTVTVTLNGQTYQGVVQPDGTWSVTVPAANVGALADG 743	Qy 594 DYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATL 644 :
QY 594 DYTFQLKVTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATL 644	Qy 645 DGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYH 690
645 DGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYH	Oy 691 FRLITVKDQQGLSSTSTLTVAVKKENNSPPRARAGGRHVLVLPNNSITLDGSRSTDDQRIV 750

5 8 5 8 5	DD 2660	Search completed: October 12, 2005, 10:22:42 Job time : 58 secs											
	Jobers: Nostoc Bp. FC 7120 Jobers: Nostoc Bp. FC 7120 Jobers: Nostoc Bp. FC 7120 Jobers: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 Jobers: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 Jobers: Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S	DNA KES 8, 205-2413, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Recession: AH2493 A;Rolecule: preliminary A;Molecule type: DNA A;Residues: 1-3083 «KUR» A;Residues: 1-3083 «KUR» A;Residues: 1-3083 «KUR» A;Residues: 1-3083 «KUR» A;Residues: 1-3083 «KUR» A;Genetics: strain PCC 7120 C;Genetics: A;Gene: a117128 A;Gene: plasmid	Ouery Match 3.4%; Score 190; DB 2; Length 3083; Best Local Similarity 21.1%; Pred. No. 0.091; Matches 167; Conservative 96; Mismatches 302; Indels 226; Gaps 35;	Qy 148 WGLEEWSEYXD'DYRELEKDILQPSGKQEPRGSAEYTDWG 186 	Qy 187LLPGSEGAFNSSVGDSPAVPAETQQDPBLHYLNE 220 DD 2026 YGDELLGGNLDDKLTGGGGADTLKAGLGNDTYILAAQTAGGSKIEDDGENDTLDLTDINL 2085	Qy 221 SASTPAPKLPERSVLLPLPTTPSSGEVLEKEKASQLQEQSSNSSG 265	Qy 266 KEVLMPSHSLPPASLELSSVIVEKSPVLTVTPGSTBHSIPTPAPTSAAPSESTPSELFISP 325 ::	QY 3.26 TTAPRTVKELTVSAGDNLIIILPDNEVELKAFVAPAPPVETTYNYEMNLISHPTDYQGEI 385 DD 2197 TAVPEASKGIIRLPDNTVVTVN	Qy 386 KQCHKQTLNLSQLSVGLYVFKVTVSSENAFGE-GFVNVTVKBARRVNLPPVAVVSPQLQE 444 Db 2219TTLTTQQLTSLVFVSVVNANGSAGSFSYTVSDGKGGTASQT 2259	Qy 445 LTLPLTSALIDGSQSTDDTEIVSY	Qy 469 HWEEINGPFIEEKTSVDSPVLRLSNLDPGNYSPRLTVTDSDGATNSTTAALIVNNAVD 526	QY 527 YPPVANAGPNHTITLPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQ 578	Qy 579 GVQTPYLHLSAMQEGDYTFQLKVTDSSRQOSTAXVTVIVOPENNRPPVAVAG 630

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FYHWEHVRGPSAVEMENIDKAIATVTGL---QV 686
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